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OM protein - protein search, using sw mode!

Run on: November 13, 2002, 13:40:23 ; Search time 14 Seconds
(without alignments)

8.407 Million cell updates/sec
Title: US-09-697-590-2.COPY-292-295
Perfect score: 21

Sequence: 1 HARL 4

Scoring table: BLOSUM62
GapOp 10.0 , GapExt 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMBO.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMBO.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMBO.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMBO.pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMBO.pep: *
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID

Description

Result No.	Score	Query	Length	DB	ID	Description
1	21	100.0	15	4	US-09-347-504-66	Sequence 66, Appl
2	21	100.0	17	1	US-09-399-646-B	Sequence 8, Appl
3	21	100.0	17	1	US-09-507-321-B	Sequence 8, Appl
4	21	100.0	17	2	US-09-963-240-B	Sequence 8, Appl
5	21	100.0	17	2	US-09-605-501-B	Sequence 23, Appl
6	21	100.0	51	2	US-08-870-158-23	Sequence 6, Appl
7	21	100.0	53	1	US-08-220-616-6	Sequence 6, Appl
8	21	100.0	53	4	US-08-446-648-6	Sequence 6, Appl
9	21	100.0	53	5	PCT-US95-04228-6	Sequence 6, Appl
10	21	100.0	82	2	US-08-403-852D-27	Sequence 27, Appl
11	21	100.0	82	3	US-08-510-646B-28	Sequence 28, Appl
12	21	100.0	82	4	US-09-231-818-27	Sequence 27, Appl
13	21	100.0	91	2	US-09-041-125-10	Sequence 10, Appl
14	21	100.0	91	3	US-07-730-335E-10	Sequence 10, Appl
15	21	100.0	113	4	US-09-311-352B-2	Sequence 2, Appl
16	21	100.0	120	1	US-08-420-235B-29	Sequence 29, Appl
17	21	100.0	120	4	US-08-793-624-29	Sequence 29, Appl
18	21	100.0	166	5	PCT-US95-10194-29	Sequence 3657, Appl
19	21	100.0	166	4	US-09-134-001C-3657	Sequence 4, Appl
20	21	100.0	170	3	US-09-186-250-4	Sequence 8, Appl
21	21	100.0	170	3	US-09-186-250-8	Sequence 4, Appl
22	21	100.0	170	4	US-09-511-347-4	Sequence 8, Appl
23	21	100.0	170	4	US-09-511-347-8	Sequence 8, Appl
24	21	100.0	170	4	US-09-510-232A-4	Sequence 8, Appl
25	21	100.0	170	4	US-09-518-232A-8	Sequence 4, Appl
26	21	100.0	170	4	US-09-517-358A-4	Sequence 8, Appl
27	21	100.0	170	4	US-09-517-358A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-347-504-66
; Sequence 66 Application US/09347504
; Patent No. 6399075
; GENERAL INFORMATION:
; APPLICANT: HOWLEY, Peter M.
; APPLICANT: Benson, John
; APPLICANT: Kasukawa, Hiroaki
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
; FILE REFERENCE: HMV-041.01
; CURRENT APPLICATION NUMBER: US/09/347,504
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: M36A

RESULT 2
US-08-399-646-B
; Sequence 8, Application US/08399646
; Patent No. 5556781
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: TSUSAKI, Keiji
; APPLICANT: HAWATORI, Kazuko
; APPLICANT: SUGIMOTO, Yoshiyuki
; TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND
; TITLE OF INVENTION: ENZYME, TRANSFORMANT, AND THEIR PREPARATIONS AND USE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA

ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/399, 646
 FILING DATE: 07-MAR-1995
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 59834
 FILING DATE: 07-MAR-1994
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: JP 59840
 FILING DATE: 07-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25, 618
 REFERENCE/DOCKET NUMBER: KUBOTA=5

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

US-08-399-646-8

Query Match 100.0%; Score 21; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 11 HARL 14

RESULT 3

US-08-607-321-8

Query Match 100.0%; Score 21; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 11 HARL 14

RESULT 4

US-08-961-240-8

Query Match 100.0%; Score 21; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 11 HARL 14

GENERAL INFORMATION:

APPLICANT: KUBOTA, Michio
 APPLICANT: TSUZAKI, Keiji
 APPLICANT: HATTORI, Kazuko
 APPLICANT: SUGIMOTO, Toshiyuki

TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK
 STREET: 4119 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/961, 240
 FILING DATE: 30-OCT-1997
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 59840
 FILING DATE: 07-MAR-1995
 APPLICATION NUMBER: JP 59834
 FILING DATE: 07-MAR-1994

ATTORNEY/AGENT INFORMATION:
 NAME: BROWDY, Roger L.
 REGISTRATION NUMBER: 25, 618
 REFERENCE/DOCKET NUMBER: KUBOTA=5

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-961-240-8

RESULT 5

US-08-605-501-8

; Sequence 8, Application US/08605501

Patent No. 583428/

GENERAL INFORMATION:

APPLICANT: KUBOTA, Michio

APPLICANT: TSUSAKI, Keiji

APPLICANT: HATTORI, Kazuko

APPLICANT: SUGIMOTO, Toshiyuki

TITLE OF INVENTION: DNA ENCODING ENZYME, RECOMBINANT DNA AND

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: BRODY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

COMPUTER SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08-605,501

FILING DATE: 26-FEB-1996

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/399,646

FILING DATE: 07-MAR-1995

APPLICATION NUMBER: JP 59834

FILING DATE: 07-MAR-1994

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: JP 59840

FILING DATE: 07-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: BRODY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: KUBOTAA-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 248633

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-605-501-8

Query Match 100.0%; Score 21; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 25; 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 HARL 4
Db	11 HARL 14

RESULT 6

US-08-870-518-23

Sequence 23, Application US/08870518

Patent No. 5925566

GENERAL INFORMATION:

APPLICANT: Davis, Roger J.

APPLICANT: Galcheva-Garcova, Zoya

TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

COMPUTER: IBM Compatible

MEDIUM TYPE: Diskette

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08-870,518

FILING DATE: 06-JUN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/019,219

FILING DATE: 06-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Fasse, Peter J.

REGISTRATION NUMBER: 32,983

REFERENCE/DOCKET NUMBER: 04020/102001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 51 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-870-518-23

Query Match 100.0%; Score 21; DB 2; Length 51;

Best Local Similarity 100.0%; Pred. No. 75; 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 HARL 4
Db	48 HARL 51

RESULT 7

US-08-222-616-6

Sequence 6, Application US/08222616

Patent No. 5835177

GENERAL INFORMATION:

APPLICANT: Bennett, Brian D.

APPLICANT: Goeddel, David

APPLICANT: Lee, James M.

APPLICANT: Matthews, William

APPLICANT: Tsai, Siao Ping

APPLICANT: Wood, William I.

TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
 TITLE OF INVENTION: ANTIBODIES
 NUMBER OF SEQUENCES: 42
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/446,648
 FILING DATE: 08/22/1993
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/222616
 FILING DATE: 04-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0821P3PCT

PRIOR APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.

REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 821P2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 53 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

SEQUENCE CHARACTERISTICS:
 LENGTH: 53 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

US-08-222-616-6

Query Match 100.0%; Score 21; DB 1; Length 53;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 4; Conservative 0; Mismatches 0;
 Qy |||||
 Db 41 HARL 44

RESULT 8
 US-08-446-648-6
 Sequence 6, Application US/08446648
 ; GENERAL INFORMATION:
 ; PATENT NO. 6331302
 ; APPLICANT: Genentech, Inc.
 ; ATTORNEY/AGENT INFORMATION:
 ; APPLICANT: Bennett, Brian D.
 ; APPLICANT: Goeddel, David
 ; APPLICANT: Lee, James M.
 ; APPLICANT: Matthews, William
 ; APPLICANT: Tsai, Siao Ping
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04228
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/222616
 FILING DATE: 04-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 00 000
 REFERENCE/DOCKET NUMBER: 821P3PCT

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 53 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

Query Match 100.0%; Score 21; DB 1; Length 53;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 4; Conservative 0; Mismatches 0;
 Qy 1 HARL 4
 Db 41 HARL 44

RESULT 9
 PCT-US95-04228-6
 Sequence 6, Application PCT-US9504228
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; ATTORNEY/AGENT INFORMATION:
 ; APPLICANT: Bennett, Brian D.
 ; APPLICANT: Goeddel, David
 ; APPLICANT: Lee, James M.
 ; APPLICANT: Matthews, William
 ; APPLICANT: Tsai, Siao Ping
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04228
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/222616
 FILING DATE: 04-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 00 000
 REFERENCE/DOCKET NUMBER: 821P3PCT

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS: .

LENGTH: 53 amino acids

TYPE: amino acid

TOPOLOGY: linear

PCT-US95-042286

Query Match Similarity 100.0%; Score 21; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0;
Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 41 HARL 44

RESULT 10
US-08-403-852D-27

Sequence 27, Application US/08403852D

Patent No. 5891695

GENERAL INFORMATION:

APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacquier, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Debussche, Laurent

APPLICANT: De Crecy-Lagard, Valerie

APPLICANT: Jaccues, Nathalie

APPLICANT: Lacroix, Patricia

APPLICANT: Thibaut, Denis

APPLICANT: Zagorec, Monique

RESULT 11
US-08-510-646B-28
Sequence 28, Application US/08510646B
; Patent No. 6077659
; GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT-FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-510-646B-28

Query Match Similarity 100.0%; Score 21; DB 3; Length 82;

Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0;
Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 46 HARL 49

RESULT 12
US-09-231-818-27
Sequence 27, Application US/09231818
; Patent No. 6,171,846
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debusche, Laurent
APPLICANT: De Grecy-Lazard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: MSU 4.1-132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal fragment
ORIGINAL SOURCE:
ORGANISM: herpes simplex virus type 1 (HSV1)
FEATURE:
NAME/KEY: Peptide of HSV1 gene US10 polypeptide
LOCATION: 192 TO 282
OTHER INFORMATION: peptide homologous to the US10 gene
OTHER INFORMATION: polypeptide of MDV
US-09-047-125-10
Query Match 100.0%; Score 21; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HARL 4
Db 30 HARL 33

RESULT 13
US-09-047-125-10
Sequence 10, Application US/09047125
; Patent No. 5,976,877
GENERAL INFORMATION:
APPLICANT: Leland F. Velicer, Peter Brunovskis,
APPLICANT: Ireland F. Velicer, Peter Brunovskis,
TITLE OF INVENTION: Marek's Disease Herpesvirus
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb
COMPUTER: IBM PS2, Model 50
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: PC-Write 3.02
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,125
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/736,335
FILING DATE: July 25, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-132
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal fragment
ORIGINAL SOURCE:
ORGANISM: herpes simplex virus type 1 (HSV1)
FEATURE:
NAME/KEY: Peptide of HSV1 gene US10 polypeptide
LOCATION: 192 TO 282
OTHER INFORMATION: peptide homologous to the US10 gene
OTHER INFORMATION: polypeptide of MDV
US-09-047-125-10
Query Match 100.0%; Score 21; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HARL 4
Db 30 HARL 33

RESULT 14
US-07-736-335E-10
Sequence 10, Application US/07736335E
; Sequence 10, Application US/07736335E
; Patent No. 6,039,127
GENERAL INFORMATION:
APPLICANT: Leland F. Velicer, Peter Brunovskis,
TITLE OF INVENTION: Marek's Disease Herpesvirus
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 Mb
COMPUTER: IBM PS2, Model 50
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: PC-Write 3.02
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/736,335E
 FILING DATE: July 25, 1991
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Ian C. McLeod

REGISTRATION NUMBER: 20,931
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 347-4100
 TELEFAX: (517) 347-4103
 INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
 LENGTH: 91 amino acids
 TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal fragment

ORGANISM: herpes simplex virus type 1 (HSV1)

FEATURE: peptide of HSV1 gene US10 polypeptide
 LOCATION: 192 TO 282
 OTHER INFORMATION: peptide homologous to the US10 gene

US-07-736-335E-10

Query Match 100.0%; Score 21; DB 3; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 30 HARL 33

RESULT 15
 Sequence 2, Application US/09311352B
 GENERAL INFORMATION:
 APPLICANT: Webb, Donna J.
 TITLE OF INVENTION: Transforming Growth Factor-beta Binding Site
 FILE REFERENCE: 00370-02
 CURRENT APPLICATION NUMBER: US/09/311,352B
 CURRENT FILING DATE: 1999-05-13
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 113
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-311-352B-2

Query Match 100.0%; Score 21; DB 4; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 30 HARL 33

RESULT 15
 Sequence 2, Application US/09311352B
 GENERAL INFORMATION:
 APPLICANT: Gonias, Steven L.
 TITLE OF INVENTION: Transforming Growth Factor-beta Binding Site
 FILE REFERENCE: 00370-02
 CURRENT APPLICATION NUMBER: US/09/311,352B
 CURRENT FILING DATE: 1999-05-13
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 2
 LENGTH: 113
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-311-352B-2

Query Match 100.0%; Score 21; DB 4; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 30 HARL 33

RESULT 17
 Sequence 29, Application US/08793624C
 GENERAL INFORMATION:
 APPLICANT: Chang, Yuan
 TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma Virus Sequences And
 TITLE OF INVENTION: Uses Thereof
 FILE REFERENCE: 45185-C-PCT-US/JPW
 CURRENT APPLICATION NUMBER: US/08/793,624C
 CURRENT FILING DATE: 1997-02-18
 NUMBER OF SEQ ID NOS: 58
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 29
 LENGTH: 120
 TYPE: PRT
 ORGANISM: Kaposi's sarcoma-associated herpesvirus
 US-08-793-624-29

Query Match 100.0%; Score 21; DB 4; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 100 HARL 103

APPLICANT: Moore, Patrick S.
 TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
 TITLE OF INVENTION: SEQUENCES AND USES THEREOF
 NUMBER OF SEQIDNOS: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/420,235B
 FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 45185-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-420-235B-29

Query Match 100.0%; Score 21; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 100 HARL 103

RESULT 16
 Sequence 29, Application US/08420235B
 GENERAL INFORMATION:
 APPLICANT: Chang, Yuan

US-08-420-235B-29

Query Match 100.0%; Score 21; DB 4; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 100 HARL 103

RESULT 18
 PCT-US95-10194-29
 Sequence 29, Application PCTUS9510194
 ; GENERAL INFORMATION:
 ; APPLICANT: The Trustees of Columbia University in the City of New York
 ; CITY: New York
 ; STREET: 1185 Avenue of the Americas
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/10194
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28, 678
 ; REFERENCE/DOCKET NUMBER: 45185-C-PCT/JPW/MSC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 278-0400
 ; TELEFAX: (212) 391-0525
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 120 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ;
 PCT-US95-10194-29

Query Match 100.0%; Score 21; DB 5; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Mismatches 0;
 Matches 4; Conservative 0; Gaps 0;

QY 1 HARL 4
 Db 100 HARL 103

RESULT 19
 US-09-134-001C-3657
 ; Sequence 3657, Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134, 001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064, 964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055, 779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO 3657
 ; LENGTH: 166
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 ; US-09-134-001C-3657

Query Match 100.0%; Score 21; DB 4; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Query Match 100.0%; Score 21; DB 3; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02; Indels 0; Mismatches 0;
 Matches 4; Conservative 0; Gaps 0;

QY 1 HARL 4
 Db 40 HARL 43

RESULT 20
 US-09-186-250-4
 ; Sequence 4, Application US/09186250A
 ; Patent No. 6043055
 ; GENERAL INFORMATION:
 ; APPLICANT: Hsueh, Aaron
 ; TITLE OF INVENTION: Bok Genes and their Uses
 ; FILE REFERENCE: SUN-72P
 ; CURRENT APPLICATION NUMBER: US/09/186, 250A
 ; CURRENT FILING DATE: 1998-11-04
 ; EARLIER APPLICATION NUMBER: 60/064, 943
 ; EARLIER FILING DATE: 1997-11-07
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 170
 ; TYPE: PRT
 ; ORGANISM: H. sapiens
 ; US-09-186-250-8

Query Match 100.0%; Score 21; DB 3; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02; Indels 0; Mismatches 0;
 Matches 4; Conservative 0; Gaps 0;

QY 1 HARL 4
 Db 40 HARL 43

RESULT 22
 US-09-517-347-4
 ; Sequence 4, Application US/09517347
 ; Patent No. 6222017
 ; GENERAL INFORMATION:
 ; APPLICANT: Hsueh, Aaron

APPLICANT: Hsu, Sheau
 TITLE OF INVENTION: Mammalian Pro-Apoptotic Bok Genes and
 TITLE OF INVENTION: their Uses
 FILE REFERENCE: STAN-072DIV
 CURRENT APPLICATION NUMBER: US/09/517,347
 CURRENT FILING DATE: 2000-03-02
 PRIORITY NUMBER: 09/186,250
 PRIORITY FILING DATE: 1998-11-04
 PRIORITY APPLICATION NUMBER: 60/064,943
 PRIORITY FILING DATE: 1997-11-07
 NUMBER OF SEQ ID NOS: 18
 SEQ ID NO 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 170
 TYPE: PRT
 ORGANISM: r.rattus
 US-09-517-347-4

Query Match 100.0%; Score 21; DB 4; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db 40 HARL 43

RESULT 23
 US-09-517-347-8
 Sequence 8, Application US/09517347
 ; GENERAL INFORMATION:
 ; APPLICANT: Hsueh, Aaron
 ; TITLE OF INVENTION: Mammalian Pro-Apoptotic Bok Genes and
 ; TITLE OF INVENTION: their Uses
 ; FILE REFERENCE: STAN-072DIV
 ; CURRENT APPLICATION NUMBER: US/09/517,347
 ; CURRENT FILING DATE: 2000-03-02
 ; PRIORITY NUMBER: 09/186,250
 ; PRIORITY FILING DATE: 1998-11-04
 ; PRIORITY APPLICATION NUMBER: 60/064,943
 ; PRIORITY FILING DATE: 1997-11-07
 ; NUMBER OF SEQ ID NOS: 18
 ; SEQ ID NO 8
 ; LENGTH: 170
 ; TYPE: PRT
 ; ORGANISM: H. sapiens
 ; US-09-517-347-8

Query Match 100.0%; Score 21; DB 4; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db 40 HARL 43

RESULT 24
 US-09-518-232A-4
 Sequence 4, Application US/09518232A
 ; Patent No. 6222017
 ; GENERAL INFORMATION:
 ; APPLICANT: Hsueh, Aaron J.W.
 ; TITLE OF INVENTION: Mammalian Pro-Apoptotic Bok Genes and
 ; FILE REFERENCE: STAN072DIV3
 ; CURRENT APPLICATION NUMBER: US/09/518,232A
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIORITY NUMBER: 09/186,250
 ; PRIORITY FILING DATE: 1998-11-04
 ; PRIORITY APPLICATION NUMBER: 60/064,943
 ; PRIORITY FILING DATE: 1997-11-07
 ; NUMBER OF SEQ ID NOS: 18
 ; SEQ ID NO 4
 ; LENGTH: 170
 ; TYPE: PRT
 ; ORGANISM: H. sapiens
 ; US-09-518-232A-8

Query Match 100.0%; Score 21; DB 4; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db 40 HARL 43

RESULT 25
 US-09-518-232A-8
 Sequence 8, Application US/09518232A
 ; Patent No. 6376247
 ; GENERAL INFORMATION:
 ; APPLICANT: Hsueh, Aaron J.W.
 ; TITLE OF INVENTION: Mammalian Pro-Apoptotic Bok Genes and
 ; FILE REFERENCE: STAN072DIV3
 ; CURRENT APPLICATION NUMBER: US/09/518,232A
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIORITY NUMBER: 09/186,250
 ; PRIORITY FILING DATE: 1998-11-04
 ; PRIORITY APPLICATION NUMBER: 60/064,943
 ; PRIORITY FILING DATE: 1997-11-07
 ; NUMBER OF SEQ ID NOS: 18
 ; SEQ ID NO 8
 ; LENGTH: 170
 ; TYPE: PRT
 ; ORGANISM: H. sapiens
 ; US-09-518-232A-8

Query Match 100.0%; Score 21; DB 4; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db 40 HARL 43

RESULT 26
 US-09-517-358A-4
 Sequence 4, Application US/09517358A
 ; Patent No. 6437097
 ; GENERAL INFORMATION:
 ; APPLICANT: Hsueh, Aaron J.W.
 ; APPLICANT: Hsueh, Sheau Yu
 ; TITLE OF INVENTION: Mammalian Pro-Apoptotic Bok Genes and
 ; FILE REFERENCE: STAN-072DIV2
 ; CURRENT APPLICATION NUMBER: US/09/517,358A
 ; CURRENT FILING DATE: 2000-03-02
 ; PRIORITY NUMBER: 09/186,250
 ; PRIORITY FILING DATE: 1998-11-04
 ; PRIORITY APPLICATION NUMBER: 60/064,943
 ; PRIORITY FILING DATE: 1997-11-07
 ; NUMBER OF SEQ ID NOS: 18
 ; SEQ ID NO 4
 ; LENGTH: 170
 ; TYPE: PRT
 ; ORGANISM: r.rattus
 ; US-09-517-358A-4

Query Match 100.0%; Score 21; DB 4; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db 40 HARL 43

us-09-697-590-2_copy_292_295.raii

COUNTRY: U.S.A.
 ZIP: 10591
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,537A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: USN 08/406,247
 FILING DATE: 17-MAR-1995
 APPLICATION NUMBER: USN 08/144,992
 FILING DATE: 28-OCT-1993
 APPLICATION NUMBER: USN 07/736,559
 FILING DATE: 26-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Kempler, Ph.D., Gail M
 REGISTRATION NUMBER: 32,143
 REFERENCE/DOCKET NUMBER: REG 070C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 914-345-7400
 TELEX: 914-345-7721
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 192 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-469-537A-37

Query Match 100.0%; Score 21; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4 |||||
 Db 46 HARL 49

RESULT 31
 US-07-661-610C-5
 ; Sequence 5, Application US/07661610C
 ; Patent No. 5292643
 GENERAL INFORMATION:
 APPLICANT: Shibano, Yuji
 APPLICANT: Toyoda, Hideyoshi
 APPLICANT: Utsumi, Ryutaro
 APPLICANT: Ohata, Kazuaki
 TITLE OF INVENTION: Fusaric Acid Resistant Genes
 NUMBER OF SEQUENCES: 15
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 2730 Sand Hill Road
 CITY: Menlo Park
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94035

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/309,512
 FILING DATE: 29-NOV-1991
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/800,218
 FILING DATE: 29-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Boettner, Scott R.
 REGISTRATION NUMBER: 34,298
 REFERENCE/DOCKET NUMBER: 8115-008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 854-3660
 TELEX: 66141 PENNE 4:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 208 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Acetobacter xylinum

RESULT 32
 US-08-309-512-4
 ; Sequence 4, Application US/08309512
 ; Patent No. 5759828
 GENERAL INFORMATION:
 APPLICANT: Tal, Ronny
 APPLICANT: Ben-Ziman, Moshe
 APPLICANT: Gelfand, David H.
 APPLICANT: Ben-Bassat, Arie
 APPLICANT: Calhoon, Roger D.
 APPLICANT: Wong, Wing C.
 TITLE OF INVENTION: CYCLIC DIGUANYLATE METABOLIC ENZYMES
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 2730 Sand Hill Road
 CITY: Menlo Park
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94035

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/309,512
 FILING DATE: 29-NOV-1991
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/800,218
 FILING DATE: 29-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Boettner, Scott R.
 REGISTRATION NUMBER: 34,298
 REFERENCE/DOCKET NUMBER: 8115-008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 854-3660
 TELEX: 66141 PENNE 4:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 208 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Acetobacter xylinum

US-08-309-512-4

RESULT 34

US-09-199-637A-401

Sequence 401, Application US/09199637A

; Patent No. 6355411

; GENERAL INFORMATION:

; APPLICANT: Ausibel, Frederick

;

; APPLICANT: Goodman, Howard M.

;

; APPLICANT: Rahme, Laurence G.

;

; APPLICANT: Mahajan Miklos, Shalina

;

; APPLICANT: Tan, Man-Wah

;

; APPLICANT: Cao, Hui

;

; APPLICANT: Dreikard, Elana

;

; APPLICANT: Tsongalis, John

;

; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID

;

; TITLE OF INVENTION: SEQUENCES AND USES THEREOF

;

; FILE REFERENCE: 00786/361002

;

; CURRENT APPLICATION NUMBER: US/09/199,637A

;

; CURRENT FILING DATE: 1998-11-25

;

; PRIOR APPLICATION NUMBER: 60/066,517

;

; PRIOR FILING DATE: 1997-11-25

;

; NUMBER OF SEQ ID NOS: 437

;

; SOFTWARE: FastSEQ for Windows Version 4.0

;

; SEQ ID NO 401

;

; LENGTH: 209

;

; TYPE: PRT

;

; ORGANISM: Pseudomonas aeruginosa

;

; US-09-199-637A-401

;

; Query Match

;

; Best Local Similarity 100.0%; Pred. No. 3.1e+02; Length 209;

;

; Mismatches 0; Indels 0; Gaps 0;

;

; RESULT 35

US-09-186-250-2

Sequence 2, Application US/09186250A

;

; Patent No. 6043055

;

; GENERAL INFORMATION:

;

; APPLICANT: Hsueh, Aaron

;

; APPLICANT: Hsu, Sheau

;

; TITLE OF INVENTION: Bok Genes and their Uses

;

; FILE REFERENCE: SUN-72P

;

; CURRENT APPLICATION NUMBER: US/09/186,250A

;

; CURRENT FILING DATE: 1998-11-04

;

; EARLIER APPLICATION NUMBER: 60/064,943

;

; EARLIER FILING DATE: 1997-11-07

;

; NUMBER OF SEQ ID NOS: 18

;

; SOFTWARE: FastSEQ for Windows Version 3.0

;

; SEQ ID NO 2

;

; LENGTH: 213

;

; TYPE: PRT

;

; ORGANISM: r. rattus

;

; US-09-186-250-2

;

; Query Match

;

; Best Local Similarity 100.0%; Pred. No. 3.2e+02; Length 213;

;

; Mismatches 0; Indels 0; Gaps 0;

;

; RESULT 36

US-09-186-250-6

Sequence 6, Application US/09186250A

;

; Patent No. 6043055

;

; GENERAL INFORMATION:

;

; APPLICANT: Hsueh, Aaron

;

RESULT 33

PCT-US92-08756A-4

Query Match 100.0%; Score 21; DB 1; Length 208; Best Local Similarity 100.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;

; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; QY 1 HARL 4

; Db 118 HARL 121

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APPLICANT: Hsu, Sheau
 TITLE OF INVENTION: Bok Genes and their Uses
 FILE REFERENCE: SUN-72P
 CURRENT APPLICATION NUMBER: US/09/186,250A
 CURRENT FILING DATE: 1998-11-04
 EARLIER APPLICATION NUMBER: 60/064,943
 EARLIER FILING DATE: 1997-11-07
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 6
 LENGTH: 213
 TYPE: PRT
 ORGANISM: H.sapiens
 ; US-09-186-250-6

Query Match 100.0%; Score 21; DB 3; Length 213;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 37
 US-09-517-347-2
 ; Sequence 2, Application US/09517347
 ; Patent No. 6222017
 ; GENERAL INFORMATION:
 ; APPLICANT: Hsueh, Aaron
 ; TITLE OF INVENTION: Mammalian Pro-Apoptotic Bok Genes and
 ; TITLE OF INVENTION: their Uses
 ; FILE REFERENCE: STAN072DIV
 ; CURRENT APPLICATION NUMBER: US/09/517,347
 ; CURRENT FILING DATE: 2000-03-02
 ; PRIOR APPLICATION NUMBER: 09/186,250
 ; PRIOR FILING DATE: 1998-11-04
 ; PRIOR APPLICATION NUMBER: 60/064,943
 ; PRIOR FILING DATE: 1997-11-07
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 213
 ; TYPE: PRT
 ; ORGANISM: r. rattus
 ; US-09-517-347-2

Query Match 100.0%; Score 21; DB 4; Length 213;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 40 HARL 43

RESULT 39
 US-09-518-232A-2
 ; Sequence 2, Application US/09518232A
 ; Patent No. 6376247
 ; GENERAL INFORMATION:
 ; APPLICANT: Hsueh, Aaron J.W.
 ; TITLE OF INVENTION: Mammalian Pro-Apoptotic Bok Genes and
 ; TITLE OF INVENTION: Their Uses
 ; FILE REFERENCE: STAN072DIV3
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: 09/186,250
 ; PRIOR FILING DATE: 1998-11-04
 ; PRIOR APPLICATION NUMBER: 60/064,943
 ; PRIOR FILING DATE: 1997-11-07
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 213
 ; TYPE: PRT
 ; ORGANISM: r. rattus
 ; US-09-518-232A-2

Query Match 100.0%; Score 21; DB 4; Length 213;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 40 HARL 43

RESULT 40
 US-09-518-232A-6
 ; Sequence 6, Application US/09518232A
 ; Patent No. 6376247
 ; GENERAL INFORMATION:
 ; APPLICANT: Hsueh, Aaron J.W.
 ; TITLE OF INVENTION: Mammalian Pro-Apoptotic Bok Genes and
 ; TITLE OF INVENTION: Their Uses
 ; FILE REFERENCE: STAN072DIV3
 ; CURRENT APPLICATION NUMBER: US/09/518,232A
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: 09/186,250
 ; PRIOR FILING DATE: 1998-11-04
 ; PRIOR APPLICATION NUMBER: 60/064,943
 ; PRIOR FILING DATE: 1997-11-07
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 213
 ; TYPE: PRT
 ; ORGANISM: H.sapiens
 ; US-09-518-232A-6

Query Match 100.0%; Score 21; DB 4; Length 213;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 HARL 43

RESULT 41
 Sequence 2, Application US/09517358A
 Patent No. 6437097
 GENERAL INFORMATION:
 APPLICANT: Hsueh, Aaron J.W.
 APPLICANT: Hsu, Sheau Yu
 TITLE OF INVENTION: Mammalian Pro-Apoptotic Bok Genes and Their Uses
 FILE REFERENCE: STAN-072DIV2
 CURRENT APPLICATION NUMBER: US/09/517,358A
 CURRENT FILING DATE: 2000-03-02
 PRIORITY NUMBER: 09/186,250
 PRIOR FILING DATE: 1998-11-04
 PRIORITY NUMBER: 60/064,943
 PRIORITY FILING DATE: 1997-11-07
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 2
 LENGTH: 213
 ORGANISM: r. rattus
 TYPE: PRY
 US-09-517-358A-2

Query Match 100.0%; Score 21; DB 4; Length 213;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 40 HARL 43

RESULT 42
 Sequence 6, Application US/09517358A
 Patent No. 6437097
 GENERAL INFORMATION:
 APPLICANT: Hsueh, Aaron J.W.
 APPLICANT: Hsu, Sheau Yu
 TITLE OF INVENTION: Mammalian Pro-Apoptotic Bok Genes and Their Uses
 FILE REFERENCE: STAN-072DIV2
 CURRENT APPLICATION NUMBER: US/09/517,358A
 CURRENT FILING DATE: 2000-03-02
 PRIORITY NUMBER: 09/186,250
 PRIOR FILING DATE: 1998-11-04
 PRIORITY NUMBER: 60/064,943
 PRIORITY FILING DATE: 1997-11-07
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 6
 LENGTH: 213
 TYPE: PRY
 ORGANISM: H.sapiens
 US-09-517-358A-6

Query Match 100.0%; Score 21; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 102 HARL 105
 US-08-796-676-3

RESULT 44
 Sequence 8, Application US/08967364
 Patent No. 5989859
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Lal, Preeti
 APPLICANT: Giegler, Karl J.
 APPLICANT: Shah, Purvi
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: VEHICLE TRAFFICKING PROTEINS
 NUMBER OF SEQUENCES: 9
 TITLE OF INVENTION: VEHICLE TRAFFICKING PROTEINS
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA

Qy 1 HARL 4
 Db 40 HARL 43

COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 COMPUTER TYPE: Diskette
 OPERATING SYSTEM: DOS
 SOFTWARE: FastaSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/967,364
 FILING DATE: 5/28/9859ember 7, 1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Cerrone, Michael C.
 REGISTRATION NUMBER: 39,132
 REFERENCE/DOCKET NUMBER: PF-0417 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 215 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: GIG69170
 LENGTH: 215 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: GIG69170
 US-09-967-364-8
 Query Match 100.0%; Score 21; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 |||||
 Db 102 HARL 105
 RESULT 45
 US-09-368-408-8
 Sequence 8, Application US/09368408
 Patent No. 6071703
 GENERAL INFORMATION:
 APPLICANT: Bandhan, Olga
 APPLICANT: Lal, Preeti
 APPLICANT: Shah, Purvi
 APPLICANT: Guegler, Karl J.
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 COMPUTER TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastaSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/213,391
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/796,676
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0213 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 215 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 969170
 US-09-213-391-3
 Query Match 100.0%; Score 21; DB 4; Length 215;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;

matches 4; conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 102 HARL 105

RESULT 47
US-08-796-676-1
; Sequence 1, Application US/08796676
; Patent No. 5858712
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: HUMAN LEA-MOTIF DEVELOPMENTAL
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,676
FILING DATE: 4/24/1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0213 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 219 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-796-676-1

Query Match 100.0%; Score 21; DB 2; length 219;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 102 HARL 105

RESULT 48
US-09-213-391-1
; Sequence 1, Application US/09213391
; Patient No. 6281190
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: HUMAN LEA-MOTIF DEVELOPMENTAL
NUMBER OF SEQUENCES: 3
TITLE OF INVENTION: PROTEIN
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA

matches 4; conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 191 HARL 194

RESULT 49
US-09-166-350-20
; Sequence 20, Application US/09166350A
; Patent No. 6440653
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew
APPLICANT: Chen, Yao
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd
APPLICANT: Jager, Eike
APPLICANT: Knuth, Alex
TITLE OF INVENTION: Renal Cancer Associated Antigens and
TITLE OF INVENTION: Uses Therefor
FILE REFERENCE: L0461//051
CURRENT APPLICATION NUMBER: US/09/166,350A
CURRENT FILING DATE: 1998-10-05
EARLIER APPLICATION NUMBER: US/09/166,350
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 223
TYPE: PRT
ORGANISM: Homo sapiens
US-09-166-350-20

Query Match 100.0%; Score 21; DB 4; Length 223;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 191 HARL 194

RESULT 50

US-09-161-241-14
; Sequence 14, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theili, Lars E
APPLICANT: Wang, Daqiang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 224
TYPE: PRT
ORGANISM: Human
US-09-161-241-14

Query Match 100.0%; Score 21; DB 4; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 HARL 4
Db 212 HARL 215

Search completed: November 13, 2002, 13:42:36
Job time : 15 secs

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OM protein - protein search, using sw model

Run on: November 13, 2002, 13:41:44 ; Search time 10 Seconds
 (without alignments)
 6.024 Million cell updates/sec

Title: US-09-697-590-2-COPY_292_295

Perfect score: 21

Sequence: 1 HARI 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97044 seqs, 15060890 residues

Total number of hits satisfying chosen parameters: 97044

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA:
 1: /cgn2_6/ptodata/2/pupaa/us08_NEW_PUB.pep; *
 2: /cgn2_6/ptodata/2/pupaa/PCTI_NEW_PUB.pep; *
 3: /cgn2_6/ptodata/2/pupaa/us06_NEW_PUB.pep; *
 4: /cgn2_6/ptodata/2/pupaa/us06_PUBCOMB.pep; *
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 7: /cgn2_6/ptodata/2/pupaa/PCTUS_PUBCOMB.pep; *
 8: /cgn2_6/ptodata/2/pupaa/US08_PUBCOMB.pep; *
 9: /cgn2_6/ptodata/2/pupaa/us09_NEW_PUB.pep; *
 10: /cgn2_6/ptodata/2/pupaa/us09_PUBCOMB.pep; *
 11: /cgn2_6/ptodata/2/pupaa/us10_NEW_PUB.pep; *
 12: /cgn2_6/ptodata/2/pupaa/us10_PUBCOMB.pep; *
 13: /cgn2_6/ptodata/2/pupaa/us60_NEW_PUB.pep; *
 14: /cgn2_6/ptodata/2/pupaa/us60_PUBCOMB.pep; *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	32	10 US-09-864-761-37322 Sequence 37322, A
2	21	100.0	53	10 US-09-982-630-6 Sequence 6, Appli
3	21	100.0	68	10 US-09-864-761-33341 Sequence 33341, A
4	21	100.0	69	10 US-09-864-761-46505 Sequence 46505, A
5	21	100.0	76	10 US-09-925-300-1130 Sequence 1130, AP
6	21	100.0	94	10 US-09-729-674-162 Sequence 162, App
7	21	100.0	117	10 US-09-925-299-1124 Sequence 1124, App
8	21	100.0	135	10 US-09-800-739-194 Sequence 194, App
9	21	100.0	155	9 US-09-712-363-155 Sequence 155, App
10	21	100.0	170	10 US-09-582-667-4 Sequence 4, Appli
11	21	100.0	170	10 US-09-682-667-8 Sequence 8, Appli
12	21	100.0	183	10 US-09-731-872-357 Sequence 357, App
13	21	100.0	186	10 US-09-815-242-11908 Sequence 11908, A
14	21	100.0	213	10 US-09-682-667-2 Sequence 2, Appli
15	21	100.0	213	10 US-09-682-667-6 Sequence 6, Appli
16	21	100.0	216	10 US-09-750-373-22 Sequence 22, Appli
17	21	100.0	224	9 US-09-976-736-14 Sequence 14, Appli
18	21	100.0	293	10 us-09-323-998D-43 Sequence 15, Appli
19	21	100.0	293	10 us-09-323-998D-43 Sequence 43, Appli

RESULT 1
 US-09-864-761-37322
 ; Sequence 37322, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wenshang
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL IN FILE REFERENCE: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: GB 24263, 6
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30

ALIGNMENTS

sequence 13325, A
 sequence 13603, A
 sequence 14, Appli
 sequence 44, Appli
 sequence 4904, Appli
 sequence 10341, A
 sequence 11761, A
 sequence 4, Appli
 sequence 2, Appli
 sequence 12071, A
 sequence 5116, Appli
 sequence 253, Appli
 sequence 4, Appli
 sequence 1635, Appli
 sequence 2, Appli
 sequence 2, Appli
 sequence 38, Appli

PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234, 687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608, 408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774, 203
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
 SEQ ID NO: 37322
 LENGTH: 32
 TYPE: PRT

ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AL049633; 3
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.3
 OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL = 3.6
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.5
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.1
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9
 OTHER INFORMATION: EXPRESSED IN HEA, SIGNAL = 3.5
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.3

US-09-982-610-6
 Query Match, Best Local Similarity 100.0%; Score 21; DB 10; Length 32;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 US-09-982-610-6
 ; Sequence 6, Application US/099B2610
 ; Patent No. US200214420A1
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 Bennett, Brian D.
 Goeddel, David
 Lee, James M.
 Matthews, William
 Tsai, Siao Ping
 Wood, William T.
 TITLE OF INVENTION: PROBIN TYROSINE KINASE AGONIST ANTIBODIES
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94030

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Winpatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/982, 610
 FILING DATE: 17-OCT-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/446, 648
 FILING DATE: 1996-MAY-23
 APPLICATION NUMBER: 08/22616
 FILING DATE: 04-APR-1994
 ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0821P3PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1994
 TELEFAX: 910/371-7168
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 53 amino acids
 TOPLOGY: Linear
 TYPE: Amino Acid
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-982-610-6
 Query Match, Best Local Similarity 100.0%; Score 21; DB 10; Length 53;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 US-09-864-761-33341
 ; Sequence 3341, Application US/09864761
 ; Patent No. US2002048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Anonmax X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 PRIOR FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180, 312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207, 456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632, 366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263, 6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236, 359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00660
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608, 408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774, 203

PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annotax Sequence Listing Engine vers. 1.1
 SEQ ID NO: 33341
 LENGTH: 68
 TYPE: PRT
 ORGANISM: Homo sapiens

FEATURE:
 OTHER INFORMATION: MAP TO AC000353.21
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.6
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.4
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
 OTHER INFORMATION: EST_HUMAN HIT: A1934403.1, EVALUE 3.00e-07
 OTHER INFORMATION: SWISSPROT HIT: O76082, EVALUE 1.00e-06
 US-09-864-761-3341

Query Match 100.0%; Score 21; DB 10; Length 68;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 10 HARL 13

RESULT 4
 US-09-864-761-46505

; Sequence 46505, Application US/09864761
 ; Patent No. US20020048763A1
 GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wenheng

TITLE OF INVENTION: HUMAN GENOMS-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aeomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SEQ ID NO 46505
 LENGTH: 69
 TYPE: PRT
 ORGANISM: Homo sapiens

FEATURE:
 OTHER INFORMATION: MAP TO AL034343.17
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3.6
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.2
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.9
 OTHER INFORMATION: SWISSPROT HIT: P25006, EVALUE 4.00e-34
 OTHER INFORMATION: EST_HUMAN HIT: AUI24791.1, EVALUE 5.00e-33
 US-09-864-761-46505

Query Match 100.0%; Score 21; DB 10; Length 69;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 50 HARL 53

RESULT 5
 US-09-925-300-1130
 ; Sequence 1130, Application US/09925300
 ; Patent No. US2002015168A1
 GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

CURRENT APPLICATION NUMBER: US/09/925,300
 CURRENT FILING DATE: 2001-08-10
 PRIOR APPLICATION NUMBER: PCT/US00/05988
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 1890
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1130
 LENGTH: 76
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-925-300-1130

Query Match 100.0%; Score 21; DB 10; Length 76;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 Db 25 HARL 28

RESULT 6
 US-09-729-674-162
 ; Sequence 162, Application US/097295674
 ; Patent No. US2001003935A1

GENERAL INFORMATION:
 ;
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John M.
 ; APPLICANT: Lavallie, Edward R.
 ; APPLICANT: Collins-Racie, Lisa A.
 ; APPLICANT: Evans, Cheryl
 ; APPLICANT: Merberg, David
 ; APPLICANT: Tracy, Maurice
 ; APPLICANT: Agostino, Michael J.
 ; APPLICANT: Steininger II, Robert J.
 ; APPLICANT: Spaulding, Vicki
 ; APPLICANT: Wong, Gordon G.
 ; APPLICANT: Clark, Hilary
 ; APPLICANT: Fechtel, Kim
 ; APPLICANT: Genetics Institute, Inc.

TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

FILE REFERENCE: 6055-64X

CURRENT APPLICATION NUMBER: US/09/729,674

CURRENT FILING DATE: 2000-12-04

PRIOR FILING DATE: 2000-03-30

NUMBER OF SEQ ID NOS: 283

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 162

LENGTH: 94

TYPE: PRT

ORGANISM: Homo sapiens

US-09-729-674-162

Query Match 100.0%; Score 21; DB 10; Length 94;
 Best Local Similarity 100.0%; Pred. No. 68; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 HARL 4

Db 30 HARL 33

RESULT 7

US-09-925-299-1124
 Sequence 1124, Application US/09925299
 Patent No. US20020055627A1

GENERAL INFORMATION:
 ;
 ; APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PAI02

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-03-10

PRIOR APPLICATION NUMBER: PCT/US00/05883

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1556

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 1124

LENGTH: 117

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: NAME/KEY: SITE

LOCATION: (7)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (87)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (97)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (99)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (110)

; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

US-09-925-299-1124

Query Match 100.0%; Score 21; DB 10; Length 117;

Best Local Similarity 100.0%; Pred. No. 85; Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 HARL 4

Db 81 HARL 84

RESULT 8

US-09-800-729-194

Sequence 194, Application US/09800729

Patent No. US20030068319A1

GENERAL INFORMATION:

; APPLICANT: Ni et al.

TITLE OF INVENTION: 32 Human secreted proteins

FILE REFERENCE: P2044P1

CURRENT APPLICATION NUMBER: US/09/800,729

CURRENT FILING DATE: 2003-03-08

PRIOR APPLICATION NUMBER: PCT/US00/26013

PRIOR FILING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: 60/155,709

PRIOR FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 217

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 194

LENGTH: 135

TYPE: PRT

ORGANISM: Homo sapiens

US-09-800-729-194

Query Match 100.0%; Score 21; DB 10; Length 135;

Best Local Similarity 100.0%; Pred. No. 98; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 HARL 4

Db 60 HARL 63

RESULT 9

US-09-712-363-155

Sequence 155, Application US/09712363

Patent No. US20020164588A1

GENERAL INFORMATION:

; APPLICANT: Eisenberg, David

APPLICANT: Rotstein, Sergio H.

APPLICANT: Marcotte, Edward M.

TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND

INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS

FILE REFERENCE: 07419-032001

CURRENT APPLICATION NUMBER: US/09/712,363

CURRENT FILING DATE: 2000-11-13

PRIOR APPLICATION NUMBER: PCT/US00/02246

PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: 60/179,531

PRIOR FILING DATE: 2000-01-01

PRIOR APPLICATION NUMBER: 60/117,844

PRIOR FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: 60/118,205,

PRIOR FILING DATE: 1999-02-01

PRIOR APPLICATION NUMBER: 60/126,593

PRIOR FILING DATE: 1999-03-26

PRIOR APPLICATION NUMBER: 60/134,093

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 60/134,092

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 60/165,124

PRIOR FILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/165,086

PRIOR FILING DATE: 1999-11-12
 NUMBER OF SEQ ID NOS: 292
 SOFTWARE: FASTSEQ FOR Windows Version 4.0
 SEQ ID NO: 155
 LENGTH: 155
 TYPE: PRT
 ORGANISM: Mycobacterium tuberculosis
 US-09-712-363-155

Query Match		Score 21;	DB 9;	Length 155;	
Best Local Similarity	100.0%	Pred. No. 1.1e+02;		Mismatches 0;	Indels 0;
Matches 4;	Conservative 0;			Gaps 0;	
Qy	1 HARL 4				
Db	104 HARL 107				

RESULT 10
 Sequence 4, Application US/09682667
 ;
 US-09-682-667-4
 ;
 Patent No. US20020076794A1
 ;
 GENERAL INFORMATION:
 ;
 APPLICANT: Hsueh, Aaron J.W.
 ;
 TITLE OF INVENTION: MAMMALIAN PRO-APOPTOTIC BOK GENES AND
 TITLE OF INVENTION: THEIR USES
 FILE REFERENCE: STAN072CON
 CURRENT APPLICATION NUMBER: US/09/682,667
 CURRENT FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: 09/517,358
 PRIOR FILING DATE: 2000-03-02
 PRIOR APPLICATION NUMBER: 09/186,250
 PRIOR FILING DATE: 1998-11-04
 PRIOR APPLICATION NUMBER: 60/064,943
 PRIOR FILING DATE: 1997-11-07
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 170
 TYPE: PRT
 ORGANISM: r. rattus
 US-09-682-667-4

Query Match		Score 21;	DB 10;	Length 170;	
Best Local Similarity	100.0%	Pred. No. 1.2e+02;		Mismatches 0;	Indels 0;
Matches 4;	Conservative 0;			Gaps 0;	
Qy	1 HARL 4				
Db	40 HARL 43				

RESULT 11
 Sequence 8, Application US/09682667
 ;
 US-09-682-667-8
 ;
 Patent No. US20020076794A1
 ;
 GENERAL INFORMATION:
 ;
 APPLICANT: Hsueh, Aaron J.W.
 ;
 TITLE OF INVENTION: MAMMALIAN PRO-APOPTOTIC BOK GENES AND
 TITLE OF INVENTION: THEIR USES
 FILE REFERENCE: STAN072CON
 CURRENT APPLICATION NUMBER: US/09/682,667
 CURRENT FILING DATE: 2001-10-05
 PRIOR APPLICATION NUMBER: 09/517,358
 PRIOR FILING DATE: 2000-03-02
 PRIOR APPLICATION NUMBER: 09/186,250
 PRIOR FILING DATE: 1998-11-04
 PRIOR APPLICATION NUMBER: 60/064,943
 PRIOR FILING DATE: 1997-11-07
 NUMBER OF SEQ ID NOS: 18

Query Match		Score 21;	DB 10;	Length 170;	
Best Local Similarity	100.0%	Pred. No. 1.2e+02;		Mismatches 0;	Indels 0;
Matches 4;	Conservative 0;			Gaps 0;	
Qy	1 HARL 4				
Db	40 HARL 43				

RESULT 12
 Sequence 357, Application US/09731872
 ;
 US-09-731-872-357
 ;
 Patent No. US20020102604A1
 ;
 GENERAL INFORMATION:
 ;
 APPLICANT: Dumas Milne Edwards, Jean Baptiste
 APPLICANT: Bouquelert, Lydie
 APPLICANT: Jobert, Severin
 TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEIN
 FILE REFERENCE: 78.US3.REG
 CURRENT APPLICATION NUMBER: US/09/731,872
 CURRENT FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: US 60/169,629
 PRIOR FILING DATE: 1999-12-08
 PRIOR APPLICATION NUMBER: US 60/187,470
 PRIOR FILING DATE: 2000-03-06
 NUMBER OF SEQ ID NOS: 482
 SOFTWARE: Patent.pm
 SEQ ID NO 357
 LENGTH: 183
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SIGNAL
 LOCATION: -47..-1

Query Match		Score 21;	DB 10;	Length 183;	
Best Local Similarity	100.0%	Pred. No. 1.3e+02;		Mismatches 0;	Indels 0;
Matches 4;	Conservative 0;			Gaps 0;	
Qy	1 HARL 4				
Db	143 HARL 146				

RESULT 13
 Sequence 11908, Application US/09815242
 ;
 US-09-815-242-11908
 ;
 Patent No. US2002020061509A1
 ;
 GENERAL INFORMATION:
 ;
 APPLICANT: Baselbeck, Robert
 APPLICANT: Ohlen, Karl L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELTRA.01IA
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11908
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-815-242-11908
Query Match 100.0%; Score 21; DB 10; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HARL 4
Db 13 HARL 16
|||||
RESULT 14
; Sequence 2, Application US/09682667
; Patent No. US20020076794A1
GENERAL INFORMATION:
; APPLICANT: Hsueh, Aaron J.W.
; APPLICANT: Hsueh, Sheau Yu
; TITLE OF INVENTION: MAMMALIAN PRO-APOPTOTIC BOK GENES AND
; TITLE OF INVENTION: THEIR USES
; FILE REFERENCE: STAN072CON
; CURRENT APPLICATION NUMBER: US/09/682,667
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/517,358
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 09/186,250
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/064,943
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 213
; TYPE: PRT
; ORGANISM: r. rattus
; US-09-682-667-2
Query Match 100.0%; Score 21; DB 10; Length 213;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HARL 4
Db 40 HARL 43
|||||
RESULT 15
; Sequence 22, Application US/09750373
; Patent No. US20030062013A1
GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Hiebsch, Ronald
; APPLICANT: Ruff, Valerie
; APPLICANT: Linneberg, Elena
; APPLICANT: Paredi, Luis A.
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: No. US20020062013A1 e1 G Protein Coupled Receptors
; FILE REFERENCE: PHRM 0300
; CURRENT APPLICATION NUMBER: US/09/750,373
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/219,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/173,339
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/224,321
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/200,534
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/239,062
; PRIOR FILING DATE: 2000-10-09
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-750-373-22
Query Match 100.0%; Score 21; DB 10; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HARL 4
Db 70 HARL 73
|||||
RESULT 17
; Sequence 6, Application US/09682667
; Patent No. US20020076794A1
GENERAL INFORMATION:
; APPLICANT: Hsueh, Aaron J.W.
; APPLICANT: Hsueh, Sheau Yu
; TITLE OF INVENTION: MAMMALIAN PRO-APOPTOTIC BOK GENES AND
; TITLE OF INVENTION: THEIR USES
; FILE REFERENCE: STAN072CON
; CURRENT APPLICATION NUMBER: US/09/682,667

Sequence 14, Application US/09976736
; Patent No. US20020161178A1
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Laird E
; APPLICANT: Wang, Daqiang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/976,736
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US/09/161,241
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 14
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Human
; US-09-976-736-14

RESULT 18
US-09-323-998D-15
; Sequence 15, Application US/09323998D
; Patent No. US20020102631A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM JR., FRANCIS X.
; TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 108172-09019
; CURRENT APPLICATION NUMBER: US/09/323,998D
; CURRENT FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 09/088,724
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 09/088,725
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 08/937,155
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: 08/624,125
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 15
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Haematococcus pluvialis
; US-09-323-998D-15

Query Match 100.0%; Score 21; DB 9; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 212 HARL 215

RESULT 18
US-09-323-998D-43
; Sequence 43, Application US/09323998D
; Patent No. US20020102631A1
; GENERAL INFORMATION:
; APPLICANT: SUN, ZAIREN
; TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 108172-09019
; CURRENT APPLICATION NUMBER: US/09/323,998D
; CURRENT FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 09/088,724
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 09/088,725
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 08/937,155
; PRIOR FILING DATE: 1997-09-25
; PRIOR APPLICATION NUMBER: 08/624,125
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 43
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-323-998D-43

Query Match 100.0%; Score 21; DB 10; Length 293;
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 25 HARL 28

RESULT 20
US-09-815-242-13325
; Sequence 13325, Application US/09815242
; Patent No. US2002006156A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA_01IA
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 13325
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
; US-09-815-242-13325

Query Match 100.0%; Score 21; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;

RESULT 21
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 US-09-815-242-13603
 ; Sequence 13603, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; PROKARYOTES
 ; FILE REFERENCE: ELITRA.011A
 ; CURRENT APPLICATION NUMBER: US/09/815, 242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191, 078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/066, 848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207, 727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242, 578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253, 625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257, 931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269, 308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 13603
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 ; US-09-815-242-13603

RESULT 22
 Query Match 100.0%; Score 21; DB 10; Length 298;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 Db 147 HARL 150

RESULT 23
 US-09-323-998D-44
 ; Sequence 44, Application US/09323998D
 ; Patent No. US20020102631A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CUNNINGHAM JR., FRANCIS X.
 ; TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
 ; FILE REFERENCE: 108172-0919
 ; CURRENT APPLICATION NUMBER: US/09/323, 998D
 ; CURRENT FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 09/088, 724
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 09/088, 725
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 08/937, 155
 ; PRIOR FILING DATE: 1997-07-25
 ; PRIOR APPLICATION NUMBER: 08/624, 125
 ; PRIOR FILING DATE: 1996-03-29
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 44
 ; LENGTH: 305
 ; TYPE: PRT
 ; ORGANISM: Haematococcus pluvialis
 ; US-09-323-998D-44

RESULT 24
 US-09-815-242-4904
 ; Sequence 4904, Application US/09815242
 ; Patent No. US20020061569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Karl L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 ; TITLE OF INVENTION: Identification of Essential Genes in
 ; PROKARYOTES
 ; FILE REFERENCE: ELITRA.011A

PRIOR APPLICATION NUMBER: PCT/ US95/08745
; PRIOR FILING DATE: 1995-07-12
; PRIOR APPLICATION NUMBER: US 08/274,215
; PRIOR FILING DATE: 1994-07-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 14
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-361-655-14

Query Match 100.0%; Score 21; DB 9; Length 350;
; Best Local Similarity 100.0%; Pred. No. 2.6e+02;
; Matches 4; Conservative 0; Mismatches 0;
; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 123 HARL 126

RESULT 28
; Sequence 2, Application US/09860351
; Patent No. US20020077463A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 16105, A NOVEL PROTEIN HUMAN PHOSPHATASE
; TITLE OF INVENTION AND USES THEREFOR
; FILE REFERENCE: 38155-20013.00
; CURRENT APPLICATION NUMBER: US 09/860,351
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/205,260
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-860-351-2

Query Match 100.0%; Score 21; DB 9; Length 350;
; Best Local Similarity 100.0%; Pred. No. 2.6e+02;
; Matches 4; Conservative 0; Mismatches 0;
; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 142 HARL 145

RESULT 29
; Sequence 12071, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Hazelbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.01IA
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5116
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-815-242-5116

Query Match 100.0%; Score 21; DB 10; Length 359;
; Best Local Similarity 100.0%; Pred. No. 2.6e+02;
; Matches 4; Conservative 0; Mismatches 0;
; Indels 0; Gaps 0;

Qy 1 HARL 4

```

Db 276 HARL 279
; |||
; Sequence 4, Application US/09973963
; Patent No. US20020106676A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Diseases
; CURRENT APPLICATION NUMBER: US/09/973,963
; CURRENT FILING DATE: 2001-10-17
; PRIORITY APPLICATION NUMBER: US 60/240,790
; PRIORITY FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-973-963-4

Query Match          100.0%; Score 21; DB 10; Length 370;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy    1 HARL 4
Db 311 HARL 314

RESULT 32
US-09-973-941-4
; Sequence 4, Application US/09973941
; Patent No. US2002016655A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,941
; CURRENT FILING DATE: 2001-10-11
; PRIORITY APPLICATION NUMBER: US 60/240,790
; PRIORITY FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-973-941-4

Query Match          100.0%; Score 21; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy    1 HARL 4
Db 311 HARL 314

RESULT 33
US-09-973-941-4
; Sequence 4, Application US/09973941
; Patent No. US2002016655A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Diseases
; CURRENT APPLICATION NUMBER: US/09/973,941
; CURRENT FILING DATE: 2001-04-11
; PRIORITY APPLICATION NUMBER: US 60/304,775
; PRIORITY FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-973-941-4

Query Match          100.0%; Score 21; DB 10; Length 370;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy    1 HARL 4
Db 311 HARL 314

RESULT 32
US-09-973-941-4
; Sequence 4, Application US/09973941
; Patent No. US2002016655A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,941
; CURRENT FILING DATE: 2001-04-11
; PRIORITY APPLICATION NUMBER: US 60/240,790
; PRIORITY FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-973-941-4

Query Match          100.0%; Score 21; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy    1 HARL 4
Db 311 HARL 314

RESULT 33
US-09-973-941-4
; Sequence 4, Application US/09973941
; Patent No. US2002016655A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Diseases
; CURRENT APPLICATION NUMBER: US/09/973,941
; CURRENT FILING DATE: 2001-04-11
; PRIORITY APPLICATION NUMBER: US 60/304,775
; PRIORITY FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 253
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-973-941-4

Query Match          100.0%; Score 21; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy    1 HARL 4
Db 174 HARL 177

RESULT 34
US-09-973-064-4
; Sequence 4, Application US/09973064
; Patent No. US20020106773A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,064
; CURRENT FILING DATE: 2001-10-10
; PRIORITY APPLICATION NUMBER: US 60/240,790
; PRIORITY FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-973-064-4

Query Match          100.0%; Score 21; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy    1 HARL 4
Db 174 HARL 177

RESULT 35
US-09-973-077-4
; Sequence 4, Application US/09973077
; Patent No. US2002014799A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Diseases
; CURRENT APPLICATION NUMBER: US/09/973,077
; CURRENT FILING DATE: 2001-10-17
; PRIORITY APPLICATION NUMBER: US 60/240,790
; PRIORITY FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-973-077-4

Query Match          100.0%; Score 21; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0;
Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy    1 HARL 4
Db 174 HARL 177

RESULT 33
US-09-973-963-4

```

FILE REFERENCE: Protein Interactions in ND

CURRENT APPLICATION NUMBER: US/09/973,077

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/240,790

PRIOR FILING DATE: 2000-10-17

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 4

LENGTH: 372

TYPE: PRT

ORGANISM: Homo sapiens

US-09-973-077-4

Query Match 100.0%; Score 21; DB 10; Length 372;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 HARL 4 |||||

Db 174 HARL 177

RESULT 36

US-09-973-063-4

Sequence 4, Application US/09973063

Patent No. US2002115119A1

GENERAL INFORMATION:

APPLICANT: Roch, Jean-Marc

APPLICANT: Bartel, Paul L.

APPLICANT: Heichman, Karen

TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative Disease

FILE REFERENCE: Protein Interactions in ND

CURRENT APPLICATION NUMBER: US/09/973,063

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/240,790

PRIOR FILING DATE: 2000-10-17

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 4

LENGTH: 372

TYPE: PRT

ORGANISM: Homo sapiens

US-09-973-063-4

Query Match 100.0%; Score 21; DB 10; Length 372;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 HARL 4 |||||

Db 174 HARL 177

RESULT 38

US-09-975-072-4

Sequence 4, Application US/09975072

Patent No. US20030115607A1

GENERAL INFORMATION:

APPLICANT: Roch, Jean-Marc

APPLICANT: Bartel, Paul L.

APPLICANT: Heichman, Karen

TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative Disease

FILE REFERENCE: Protein Interactions in ND

CURRENT APPLICATION NUMBER: US/09/975,072

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 60/240,790

PRIOR FILING DATE: 2000-10-17

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 4

LENGTH: 372

TYPE: PRT

ORGANISM: Homo sapiens

US-09-975-072-4

Query Match 100.0%; Score 21; DB 10; Length 372;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 4; Conservative 0; Mismatches 0;

Indels 0; Gaps 0;

Qy 1 HARL 4 |||||

Db 174 HARL 177

RESULT 39

US-09-972-038-4

Sequence 4, Application US/09972038

Patent No. US200211915A1

GENERAL INFORMATION:

APPLICANT: Roch, Jean-Marc

APPLICANT: Bartel, Paul L.

APPLICANT: Heichman, Karen

TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative Disease

FILE REFERENCE: Protein Interactions in ND

CURRENT APPLICATION NUMBER: US/09/972,038

CURRENT FILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: US 60/240,790

PRIOR FILING DATE: 2000-10-17

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 4

LENGTH: 372

TYPE: PRT

ORGANISM: Homo sapiens

US-09-972-038-4

Query Match 100.0%; Score 21; DB 10; Length 372;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 174 HARL 177

RESULT 40
US-09-972-757-4
; Sequence 4, Application US/09972757
; Patent No. US2002011997A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Barrel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/972,757
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-972-757-4

Query Match 100 %; Score 21; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 174 HARL 177

RESULT 41
US-09-973-965-4
; Sequence 4, Application US/09973965
; Patent No. US20020124273A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Heichman, Karen
; APPLICANT: Barrel, Paul L.
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,965
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-973-965-4

Query Match 100 %; Score 21; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 174 HARL 177

RESULT 42
US-09-925-300-1655
; Sequence 2, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1800
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 1655
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (144)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (290)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (325)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; US-09-925-300-1655

Query Match 100.0%; Score 21; DB 10; Length 373;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 175 HARL 178

RESULT 43
US-09-864-666-2
; Sequence 2, Application US/09964666
; Patent No. US20020104108A1
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; Wands, Jack R.
; TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sternlieb, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/964,666
; FILING DATE: 28-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609,4370000

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-964-666-2

Query Match 100.0%; Score 21; DB 10; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HARL 4
Db 292 HARL 295

RESULT 44
US-09-964-412-2

Sequence 2, Application US/09964412
Patent No. US20020123391A1
GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne
TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

GENERAL INFORMATION:
APPLICANT: Falb, Dean A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

GENERAL INFORMATION:
APPLICANT: Falb, Dean A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

GENERAL INFORMATION:
APPLICANT: Falb, Dean A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

GENERAL INFORMATION:
APPLICANT: Falb, Dean A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

GENERAL INFORMATION:
APPLICANT: Falb, Dean A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

GENERAL INFORMATION:
APPLICANT: Falb, Dean A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

GENERAL INFORMATION:
APPLICANT: Falb, Dean A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

Db 292 HARL 295

RESULT 45
US-09-371-900-38
Sequence 38, Application US/09371900
Patent No. US20020137700A1
GENERAL INFORMATION:
APPLICANT: Falb, Dean A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

GENERAL INFORMATION:
APPLICANT: Falb, Dean A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

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COUNTRY: USA
ZIP: 10036-2711

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ZIP: 10036-2711

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ZIP: 10036-2711

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STATE: New York
COUNTRY: USA
ZIP: 10036-2711

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COUNTRY: USA
ZIP: 10036-2711

GENERAL INFORMATION:
APPLICANT: Falb, Dean A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

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STATE: New York
COUNTRY: USA
ZIP: 10036-2711

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ZIP: 10036-2711

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STATE: New York
COUNTRY: USA
ZIP: 10036-2711

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APPLICANT: Falb, Dean A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

QY 1 HARL 4
Db 173 HARL 176

RESULT 46
US-09-924,417-59
Sequence 59, Application US/0924417
Patent No. US20020142441A1
GENERAL INFORMATION:
APPLICANT: Falb, Dean A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE

NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEO Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/924,417
 FILING DATE: 07-Aug-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/034,286
 FILING DATE: 04-Mar-1998
 FILING DATE: 06-Jun-1997
 APPLICATION NUMBER: 08/7799,910
 FILING DATE: 13-Feb-1997
 APPLICATION NUMBER: 60/011,787
 FILING DATE: 16-Feb-1996
 APPLICATION NUMBER: 08/5599,654
 FILING DATE: 09-Feb-1996
 APPLICATION NUMBER: 08/485,573
 FILING DATE: 07-Jun-1995
 APPLICATION NUMBER: 08/386,844
 FILING DATE: 10-Feb-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Cotuzzi, Laura A.
 REFERENCE/DOCKET NUMBER: 30-742
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)909090
 TELEFAX: (212)8699741
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:
 LENGTH: 375 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: unknown

MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 59:
 US-09-924-417-59

Query Match 100.0%; Score 21; DB 10; Length 375;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 HARL 4
 Db |||
 Db 173 HARL 176

RESULT 47
 US-09-833-745-9

Sequence 9, Application US/09833745
 Patent No. US20020052038A1
 GENERAL INFORMATION:
 APPLICANT: ROBERTS, JOSEPH
 APPLICANT: SETHURAMAN, NATARAJAN
 APPLICANT: MACALLISTER, THOMAS
 APPLICANT: MACALLISTER, THOMAS
 TITLE OF INVENTION: CLONING, OVEREXPRESSION AND THERAPEUTIC USE OF
 FILE REFERENCE: 078728/106
 CURRENT APPLICATION NUMBER: US/09/833,745
 PRIOR APPLICATION NUMBER: 60/197,770
 PRIOR FILING DATE: 2000-04-14
 NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 9
 LENGTH: 404
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: polypeptide

Query Match 100.0%; Score 21; DB 10; Length 404;
 Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0;
 Matches 4; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 HARL 4
 Db |||
 Db 304 HARL 307

RESULT 49
 US-09-712-363-173

Sequence 173, Application US/09712363
 Patent No. US20020164588A1
 GENERAL INFORMATION:
 APPLICANT: Eisenberg, David
 APPLICANT: Rotstein, Sergio H.
 APPLICANT: Marrotte, Edward M.
 TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
 FILE REFERENCE: 07419-032001
 CURRENT APPLICATION NUMBER: US/09/712,363
 PRIOR APPLICATION NUMBER: PCT/US00/02246
 PRIOR FILING DATE: 2000-01-28
 PRIOR APPLICATION NUMBER: 60/179,531
 PRIOR FILING DATE: 2000-02-01
 PRIOR APPLICATION NUMBER: 60/117,844
 PRIOR FILING DATE: 1999-01-29

PRIOR APPLICATION NUMBER: 60/118, 206,
 PRIOR FILING DATE: 1999-02-01
 PRIOR APPLICATION NUMBER: 60/126, 593
 PRIOR FILING DATE: 1999-03-26
 PRIOR APPLICATION NUMBER: 60/134, 093
 PRIOR FILING DATE: 1999-05-14
 PRIOR APPLICATION NUMBER: 60/134, 092
 PRIOR FILING DATE: 1999-05-14
 PRIOR APPLICATION NUMBER: 60/165, 124
 PRIOR APPLICATION NUMBER: 60/165, 086
 PRIOR FILING DATE: 1999-11-12
 NUMBER OF SEQ ID NOS: 292
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 173
 LENGTH: 410
 TYPE: PRT
 ORGANISM: *Mycobacterium tuberculosis*
 US-09-712-363-173

Query March 100.0%; Score 21; DB 9; Length 410;
 Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 HARL 4	
Db	129 HARL 132	

RESULT 50

US-09-925-301-954

; Sequence 954, Application US/09925301
 ; Patent No. US20020052308A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PAI06
 ; CURRENT APPLICATION NUMBER: US/09/925,301
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05882
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1694
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 954
 ; LENGTH: 428
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-925-301-954

Query Match 100.0%; Score 21; DB 10; Length 428;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 HARL 4	
Db	165 HARL 168	

Search completed: November 13, 2002, 13:45:32
 Job time : 11 secs

PT these diseases -
 XX
 PS Claim 1; Page 29; 53pp; English.

CC The present invention describes a neural thread protein (NTP) peptide
 CC having an amino acid sequence selected from ABB81511 to ABB81529 and
 CC their homologues, which are referred collectively as Haril peptides (I).
 CC (I) have neuroprotective, nontropic, vasoconstrictive and cerebroprotective
 CC activities, and can be used in peptide therapy. The Haril peptide
 CC sequences can be used as analogues for NTP in therapeutic or diagnostic
 CC assays by replacing NTP with the peptide in such an assay. The Haril
 CC peptides are also useful as a trap material in a diagnostic or
 CC therapeutic assay. Therefore, the Haril peptides are useful in binding
 CC assays, protein and antibody purification, therapeutics or diagnostics.
 CC In particular, the peptides are also useful for diagnosing Alzheimer's
 CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
 CC are also useful as targets for drug development for the treatment of
 CC these diseases.

CC Sequence 4 AA;

Query Match 100.0%; Score 21; DB 23; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 1 HARL 4

RESULT 2
 ABB81511
 ID ABB81511 standard; peptide; 5 AA.
 XX
 AC ABB81511;
 XX
 DT 02-SEP-2002 (first entry)
 DE Neural thread protein (NTP) peptide #1.
 KW Neural thread protein; NTP; Haril peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma;
 KW glioblastoma; ischaemia; cerebral infarction.
 OS Homo sapiens.
 XX
 PN WO200234915-A2.
 PD 02-MAY-2002.
 XX
 PF 25-OCT-2001; 2001WO-US42813.
 PR 27-OCT-2000; 2000US-0697590.
 XX
 PA (NYMO-) NYMOX PHARM CORP.
 XX
 PI Fitzpatrick J, Averback P, Focht MSS, Bibiano R;
 XX
 DR WPI; 2002-507998/54.

PT New Haril peptide sequences of the Neural Thread Protein, useful in
 PT therapeutic assays, e.g. as targets for developing drugs for treating
 PT Alzheimer's disease; ischemia or cerebral infarction, or for diagnosing
 PT these diseases -
 XX
 PS Claim 1; Page 29; 53pp; English.

XX
 CC The present invention describes a neural thread protein (NTP) peptide
 CC having an amino acid sequence selected from ABB81511 to ABB81529 and
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 CC peptides are also useful as a trap material in a diagnostic or
 CC therapeutic assay. Therefore, the Haril peptides are useful in binding
 CC assays, protein and antibody purification, therapeutic or diagnostics.
 CC In particular, the peptides are also useful for diagnosing Alzheimer's
 CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
 CC are also useful as targets for drug development for the treatment of
 CC these diseases.

CC Sequence 5 AA;
 Query Match 100.0%; Score 21; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 2 HARL 5

RESULT 3
 ABB81513
 ID ABB81513 standard; peptide; 5 AA.
 XX
 AC ABB81513;
 XX
 DT 02-SEP-2002 (first entry)
 DE Neural thread protein (NTP) peptide #3.
 KW Neural thread protein; NTP; Haril peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 OS Homo sapiens.
 XX
 PN WO200234915-A2.
 PD 02-MAY-2002.
 XX
 PR 25-OCT-2001; 2001WO-US42813.
 PR 27-OCT-2000; 2000US-0697590.
 XX
 PA (NYMO-) NYMOX PHARM CORP.
 XX
 PI Fitzpatrick J, Averback P, Focht MSS, Bibiano R;
 XX
 DR WPI; 2002-507998/54.

PT New Haril peptide sequences of the Neural Thread Protein, useful in
 PT therapeutic assays, e.g. as targets for developing drugs for treating
 PT Alzheimer's disease; ischemia or cerebral infarction, or for diagnosing
 PT these diseases -
 XX
 PS Claim 1; Page 29; 53pp; English.

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 CC having an amino acid sequence selected from ABB81511 to ABB81529 and
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 CC activities, and can be used in peptide therapy. The Haril peptide
 CC sequences can be used as analogues for NTP in therapeutic or diagnostic
 CC assays by replacing NTP with the peptide in such an assay. The Haril
 CC peptides are also useful as a trap material in a diagnostic or
 CC therapeutic assay. Therefore, the Haril peptides are useful in binding
 CC assays, protein and antibody purification, therapeutic or diagnostics.
 CC In particular, the peptides are also useful for diagnosing Alzheimer's
 CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
 CC are also useful as targets for drug development for the treatment of
 CC these diseases.

CC these diseases.
 XX
 SQ Sequence 5 AA:

Db |||||
 1 HARL 4

RESULT 4
 ABB81514
 ID ABB81514 standard; peptide; 6 AA.
 XX
 AC ABB81514;
 XX
 DT 02-SEP-2002 (first entry)
 DE Neural thread protein (NTP) peptide #4.

XX
 Neural thread protein; NTP; Harlil peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 XX
 OS Homo sapiens.

XX
 Neural thread protein (NTP) peptide #11.
 XX
 RESULT 5
 ABB81521
 ID ABB81521 standard; peptide; 6 AA.
 XX
 AC ABB81521;
 XX
 DT 02-SEP-2002 (first entry)

XX
 Neural thread protein (NTP) peptide #11.
 XX
 DR 02-MAY-2002.
 XX
 PR 25-OCT-2001; 2001WO-US42813.
 XX
 PR 27-OCT-2000; 2000US-0697590.
 XX
 PA (NYMO-) NYMOX PHARM CORP.
 XX
 PI Fitzpatrick J, Averback P, Focht MSS, Bibiano R;
 XX
 DR WPI; 2002-507998/54.

XX
 New Harlil peptide sequences of the Neural Thread Protein, useful in therapeutic assays, e.g. as targets for developing drugs for treating Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing these diseases -

XX
 PS Claim 1; Page 29; 53pp; English.

XX
 The present invention describes a neural thread protein (NTP) peptide having an amino acid sequence selected from ABB81511 to ABB81529 and their homologues, which are referred collectively as Harlil peptides (I).
 CC (I) have neuroprotective, nootropic, vasoconstrictive and cerebroprotective activities, and can be used in peptide therapy. The Harlil peptide sequences can be used as analogues for NTP in therapeutic or diagnostic assays by replacing NTP with the peptide in such an assay. The Harlil peptides are also useful as a trap material in a diagnostic or therapeutic assay. Therefore, the Harlil peptides are useful in binding assays, protein and antibody purification, therapeutics or diagnostics.

CC In particular, the peptides are also useful for diagnosing Alzheimer's disease, Down's syndrome, neuroectodermal tumours, astrocytomas, glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides are also useful as targets for drug development for the treatment of these diseases.

XX
 SQ Sequence 6 AA;

XX
 Query Match 100.0%; Score 21; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 QY 1 HARL 4
 Db |||||
 1 HARL 4

XX
 SQ Sequence 6 AA;
 XX
 The present invention describes a neural thread protein (NTP) peptide having an amino acid sequence selected from ABB81511 to ABB81529 and their homologues, which are referred collectively as Harlil peptides (I).
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CC In particular, the peptides are also useful for diagnosing Alzheimer's disease, Down's syndrome, neuroectodermal tumours, astrocytomas, glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides are also useful as targets for drug development for the treatment of these diseases.

XX
 SQ Sequence 6 AA;

XX
 Query Match 100.0%; Score 21; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4

XX
 RESULT 6
 ABB81528
 ID ABB81528 standard; peptide; 6 AA.
 XX
 AC ABB81528;

XX
 XX
 DT 02-SEP-2002 (first entry)
 XX
 DE Neural thread protein (NTP) peptide #18.
 XX
 KW Neural thread protein; NTP; Haril peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200234915-A2.
 XX
 PD 02-MAY-2002.
 XX
 PR 25-OCT-2001; 2001WO-US42813.
 XX
 PT 27-OCT-2000; 2000US-0697590.
 PA (NYMO-) NYMOX PHARM CORP.
 XX
 PI Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;
 DR WPI; 2002-507998/54.
 XX
 PT New Haril peptide sequences of the Neural Thread Protein, useful in therapeutic assays, e.g. as targets for developing drugs for treating Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing these diseases -
 XX
 PS Claim 1; Page 29; 53pp; English.
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 CC In particular, the peptides are also useful for diagnosing Alzheimer's disease, Down's syndrome, neuroectodermal tumours, astrocytomas, glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides are also useful as targets for drug development for the treatment of these diseases.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 21; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 DB 1 HARL 4
 QY 1 HARL 4
 DB 2 HARL 5
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 21; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;
 ID ABB81517 standard; peptide: 6 AA.
 ID ABB81517 standard; peptide: 7 AA.
 AC ABB81517;
 XX
 DT 02-SEP-2002 (first entry)
 XX
 DE Neural thread protein (NTP) peptide #7.
 XX
 KW Neural thread protein; NTP; Haril peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200234915-A2.
 XX
 PD 02-MAY-2002.
 XX
 PR 25-OCT-2001; 2001WO-US42813.
 XX
 PR 27-OCT-2000; 2000US-0697590.
 PA (NYMO-) NYMOX PHARM CORP.
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 PI Fitzpatrick J, Averbach P, Focht MSS, Bibiano R;
 DR WPI; 2002-507998/54.
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 CC In particular, the peptides are also useful for diagnosing Alzheimer's disease, Down's syndrome, neuroectodermal tumours, astrocytomas, glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides are also useful as targets for drug development for the treatment of these diseases.
 XX
 SQ Sequence 7 AA;
 Query Match 100.0%; Score 21; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 DB 2 HARL 5
 XX
 RESULT 8
 ABB81517
 ID ABB81517 standard; peptide: 7 AA.
 XX
 AC ABB81517;
 XX
 DT 02-SEP-2002 (first entry)
 XX
 DE Neural thread protein (NTP) peptide #7.
 XX
 KW Neural thread protein; NTP; Haril peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200234915-A2.
 XX
 PD 02-MAY-2002.
 XX
 PR 25-OCT-2001; 2001WO-US42813.
 XX
 PR 27-OCT-2000; 2000US-0697590.

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 PA (NYMO-) NYMOX PHARM CORP.
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 PI Fitzpatrick J, Averback P, Focht MSS, Bibiano R;
 XX
 DR WPI; 2002-507998/54.
 XX
 PT New Harill peptide sequences of the Neural Thread Protein, useful in therapeutic assays, e.g. as targets for developing drugs for treating Alzheimer's disease, ischaemia or cerebral infarction, or for diagnosing these diseases -
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 PS Claim 1; Page 29; 53pp; English.
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 CC (I) have neuroprotective, nootropic, vasotrophic and cerebroprotective activities, and can be used in peptide therapy. The Harill peptide sequences can be used as analogues for NTP in therapeutic or diagnostic assays by replacing NTP with the peptide in such an assay. The Harill peptides are also useful as a trap material in a diagnostic or therapeutic assay. Therefore, the Harill peptides are useful in binding assays, protein and antibody purification, therapeutics or diagnostics. In particular, the peptides are also useful for diagnosing Alzheimer's disease, Down's syndrome, neuroectodermal tumours, astrocytomas, glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides are also useful as targets for drug development for the treatment of these diseases -
 XX
 SQ Sequence 7 AA:
 Query Match 100.0%; Score 21; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 AC |||||
 Db 2 HARL 5
 RESULT 9
 ABB81518
 ID ABB81518 standard; peptide; 7 AA.
 XX
 AC ABB81518;
 XX
 DT 02-SEP-2002 (first entry)
 DE Neural thread protein (NTP) peptide #8.
 XX
 KW Neural thread protein; NTP; Harill peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200234915-A2.
 XX
 PD 02-MAY-2002.
 XX
 PR 25-OCT-2001; 2001WO-US42813.
 XX
 PA 27-OCT-2000; 2000US-0697590.
 XX
 PN (NYMO-) NYMOX PHARM CORP.
 XX
 PD 02-MAY-2002.
 XX
 PR 25-OCT-2001; 2001WO-US42813.
 XX
 PR 27-OCT-2000; 2000US-0697590.
 XX
 PA (NYMO-) NYMOX PHARM CORP.
 XX
 PT Fitzpatrick J, Averback P, Focht MSS, Bibiano R;
 XX
 PI Fitzpatrick J, Averback P, Focht MSS, Bibiano R;
 XX
 DR WPI; 2002-507998/54.
 XX
 PT New Harill peptide sequences of the Neural Thread Protein, useful in therapeutic assays, e.g. as targets for developing drugs for treating Alzheimer's disease, ischaemia or cerebral infarction, or for diagnosing these diseases -
 XX
 PS Claim 3; Page 30; 53pp; English.
 XX
 CC The present invention describes a neural thread protein (NTP) peptide having an amino acid sequence selected from ABB81511 to ABB81529 and their homologues, which are referred collectively as Harill peptides (I).
 CC (I) have neuroprotective, nootropic, vasotrophic and cerebroprotective

PT Alzheimer's disease, ischaemia or cerebral infarction, or for diagnosing these diseases -
 PT these diseases -
 XX
 PS Claim 1; Page 29; 53pp; English.
 XX
 CC The present invention describes a neural thread protein (NTP) peptide having an amino acid sequence selected from ABB81511 to ABB81529 and their homologues, which are referred collectively as Harill peptides (I).
 CC (I) have neuroprotective, nootropic, vasotrophic and cerebroprotective activities, and can be used in peptide therapy. The Harill peptide sequences can be used as analogues for NTP in therapeutic or diagnostic assays by replacing NTP with the peptide in such an assay. The Harill peptides are also useful as a trap material in a diagnostic or therapeutic assay. Therefore, the Harill peptides are useful in binding assays, protein and antibody purification, therapeutics or diagnostics. In particular, the peptides are also useful for diagnosing Alzheimer's disease, Down's syndrome, neuroectodermal tumours, astrocytomas, glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides are also useful as targets for drug development for the treatment of these diseases.
 XX
 SQ Sequence 7 AA:
 Query Match 100.0%; Score 21; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 AC |||||
 Db 2 HARL 5
 RESULT 10
 ABB81537
 ID ABB81537 standard; peptide; 8 AA.
 XX
 AC ABB81537;
 XX
 DT 02-SEP-2002 (first entry)
 DE Neural thread protein (NTP) peptide #27.
 XX
 KW Neural thread protein; NTP; Harill peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200234915-A2.
 XX
 PD 02-MAY-2002.
 XX
 PR 25-OCT-2001; 2001WO-US42813.
 XX
 PA 27-OCT-2000; 2000US-0697590.
 XX
 PN (NYMO-) NYMOX PHARM CORP.
 XX
 PD 02-MAY-2002.
 XX
 PR 25-OCT-2001; 2001WO-US42813.
 XX
 PR 27-OCT-2000; 2000US-0697590.
 XX
 PA (NYMO-) NYMOX PHARM CORP.
 XX
 PT Fitzpatrick J, Averback P, Focht MSS, Bibiano R;
 XX
 DR WPI; 2002-507998/54.
 XX
 PT New Harill peptide sequences of the Neural Thread Protein, useful in therapeutic assays, e.g. as targets for developing drugs for treating Alzheimer's disease, ischaemia or cerebral infarction, or for diagnosing these diseases -
 XX
 PS Claim 3; Page 30; 53pp; English.
 XX
 CC The present invention describes a neural thread protein (NTP) peptide having an amino acid sequence selected from ABB81511 to ABB81529 and their homologues, which are referred collectively as Harill peptides (I).
 CC (I) have neuroprotective, nootropic, vasotrophic and cerebroprotective

activities, and can be used in peptide therapy. The Harl1 peptide sequences can be used as analogues for NTP in therapeutic or diagnostic assays by replacing NTP with the peptide in such an assay. The Harl1 peptides are also useful as a trap material in a diagnostic or therapeutic assay. Therefore, the Harl1 peptides are useful in binding assays, protein and antibody purification, therapeutics or diagnostics. In particular, the peptides are also useful for diagnosing Alzheimer's disease, Down's syndrome, neuroectodermal tumours, astrocytomas, glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides are also useful as targets for drug development for the treatment of these diseases. The present sequence represents a specifically claimed peptide from the present invention.

SQ Sequence 8 AA;

Query Match 100.0%; Score 21; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HARL 4
Db 3 HARL 6

RESULT 11

AAG99428 standard; Peptide: 9 AA.
ID AAG99428;
AC AAG99428;

XX DT 01-OCT-2001 (first entry)
DE PRAME derived HLA-A*0201 binding peptide SEQ ID NO: 120.

XX ID AAG99478
XX AC AAG99478;

XX PRAME derived HLA-A*0201 binding peptide SEQ ID NO: 70.
XX DE PRAME derived HLA-A*0201 binding peptide SEQ ID NO: 120.

XX Vaccine; immune response; T cell response; epitope; proteasome;
XX KW cancer; infection.

XX OS Unidentified.

XX PN EP1118860-A1.

XX PD 25-JUL-2001.

XX PF 21-JAN-2000; 2000EP-0200242.

XX PR 21-JAN-2000; 2000EP-0200242.

XX PA (UYLE-) RIJKSUNIV LEIDEN.
XX PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.

XX PI Ossendorp F, Offringa R, Melief CJM, Kessler JH;

XX DR WPI: 2001-427158/46.

XX PS Selecting and/or producing a T cell epitope useful in a vaccine
XX PT comprises subjecting a precursor peptide or polypeptide to the action
XX PT of a 20S proteasome to determine the location of the C-terminus

XX Disclosure; Page 62; 102pp; English.

XX CC The present invention describes a method of producing T cell epitopes,

XX CC involving subjecting a precursor peptide to the action of a 20S

XX CC proteasome, in order to locate the C-terminus of said epitope. This can

XX CC be used in the production of vaccines, which can then be used to provoke

XX CC a T cell response in the treatment of diseases such as cancer and

XX CC infections. The present sequence is a peptide described in the

XX CC exemplification of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 21; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HARL 4
Db 6 HARL 9

The present invention describes a method of producing T cell epitopes, involving subjecting a precursor peptide to the action of a 20S proteasome, in order to locate the C-terminus of said epitope. This can be used in the production of vaccines, which can then be used to provoke a T cell response in the treatment of diseases such as cancer and infections. The present sequence is a peptide described in the exemplification of the invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 21; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HARL 4
Db 6 HARL 9

RESULT 13

AAG99452 standard; Peptide: 10 AA.
ID AAG99452
XX AC AAG99452;

XX DT 01-OCT-2001 (first entry)

XX DE PRAME derived HLA-A*0201 binding Peptide SEQ ID NO: 94.

XX KW Vaccine; immune response; T cell response; epitope; proteasome;

XX cancer; infection.

XX OS Unidentified.
 XX XX EP118860-A1.
 XX PD 25-JUL-2001.
 XX XX 21-JAN-2000; 2000EP-0200242.
 XX PR 21-JAN-2000; 2000EP-0200242.
 XX (WILE-) RIKKUNIV LEIDEN.
 PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
 XX Ossendorp F, Offringa R, Melief CJM, Kessler JH;
 PI WPI; 2001-427158/46.
 XX
 DR Selecting and/or producing a T cell epitope useful in a vaccine comprising subjecting a precursor peptide or polypeptide to the action of a 20S proteasome to determine the location of the C-terminus
 XX Disclosure; Page 52; 102pp; English.
 XX
 CC The present invention describes a method of producing T cell epitopes, involving subjecting a precursor peptide to the action of a 20S proteasome, in order to locate the C-terminus of said epitope. This can be used in the production of vaccines, which can then be used to provoke a T cell response in the treatment of diseases such as cancer and infections. The present sequence is a peptide described in the exemplification of the invention.
 CC Sequence 10 AA:
 XX
 Query Match 100.0%; Score 21; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 74; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 AC |||||
 DB 3 HARL 6
 RESULT 14
 ABB81536 ID ABB81536 standard; peptide; 10 AA.
 XX AC ABB81536;
 XX DT 02-SEP-2002 (first entry)
 XX DE Neural thread protein (NTP) peptide #26.
 XX KW Neural thread protein; NTP; Harlil peptide; Alzheimer's disease;
 KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
 KW hypoxia; ischaemia; cerebral infarction.
 OS Homo sapiens.
 XX PN WO20023915-A2..
 XX PD 02-MAY-2002.
 XX PF 25-OCT-2001; 2001WO-US42813.
 PR 27-OCT-2000; 2000US-0697590.
 XX PA (NYMO-) NYMOX PHARM CORP.
 XX PI Fitzpatrick J, Averback P, Focht MSS, Bibiano R;
 DR WPI; 2002-507998/44.

XX PS
 PT New Harlil peptide sequences of the Neural Thread Protein, useful in therapeutic assays, e.g. as targets for developing drugs for treating Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing these diseases.
 XX PS Claim 3; Page 30; 53pp; English.
 XX CC The present invention describes a neural thread protein (NTP) Peptide having an amino acid sequence selected from ABB81511 to ABB81529 and their homologues, which are referred collectively as Harlil peptides (I).
 CC (I) have neuroprotective, nootropic, vasoactive and cerebroprotective activities, and can be used in peptide therapy. The Harlil Peptide sequences can be used as analogues for NMP in therapeutic or diagnostic assays by replacing NTP with the peptide in such an assay. The Harlil peptides are also useful as a trap material in a diagnostic or therapeutic assay. Therefore, the Harlil peptides are useful in binding assays, protein and antibody purification, therapeutics or diagnostics. In particular, the peptides are also useful for diagnosing Alzheimer's disease, Down's syndrome, neuroectodermal tumours, astrocytomas, glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides are also useful as targets for drug development for the treatment of these diseases. The present sequence represents a specifically claimed peptide from the present invention.
 XX SQ Sequence 10 AA:
 Query Match 100.0%; Score 21; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 74; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 AC |||||
 DB 5 HARL 8
 RESULT 15
 ABB31270 ID ABB31270 standard; peptide; 12 AA.
 XX AC AAB31270;
 XX DT 20-APR-2001 (first entry)
 XX DE Peptide ligand which binds to human MUC1 protein.
 XX KW MUC1; epithelial cell mucin; tumour; MUC1 ligand; cancer.
 XX OS Synthetic.
 XX PN WO200077031-A2.
 XX PD 21-DEC-2000.
 XX PF 15-JUN-2000; 2000WO-CA0711.
 XX PR 15-JUN-1999; 99US-0139263.
 XX PA (UYHE-) UNIV HEALTH NETWORK.
 XX PI Gariepy J, Yang S;
 XX DR WPI; 2001-091388/10.
 XX PT Novel ligands that binds to MUC1, an epithelial cell mucin, useful for diagnosing, monitoring, treating and preventing cancer.
 XX PT
 XX PS Claim 15; Page 42; 60pp; English.
 XX CC The present sequence represents a peptide ligand which binds to human MUC1 protein. MUC1 is an epithelial cell mucin, which is found on, and shed from, the surface of many tumours. MUC1 peptide ligands were isolated using a phage display technique using MUC1 tandem repeats as the target. The MUC1 tandem target repeats comprise repeats of the

CC Peptide AAB31258. The ligands are useful for detecting the presence of
 CC MUC1 in a sample, to treat or prevent cancer associated with MUC1 and
 CC to prepare a medicament or diagnostic agent to treat, prevent or detect
 CC cancer associated with MUC1. By assaying for the binding between the
 CC MUC1 ligand and MUC1 in a sample diagnosis or monitoring of cancer can
 CC be carried out. The ligands may also be used to prepare antibodies.

XX Sequence 12 AA;

Query Match 100.0%; Score 21; DB 22; Length 12;
 Best Local Similarity 100.0%; Pred. No. 89; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 2 HARL 5

RESULT 16

ABB81533
 ID ABB81533 standard; peptide; 12 AA.

XX ABB81533;
 AC
 XX

DT 02-SEP-2002 (first entry)

DE Neural thread protein (NTP) peptide #23.

XX Neural thread protein; NTP; Haril peptide; Alzheimer's disease;

KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;

KW hypoxia; ischaemia; cerebral infarction.

OS Homo sapiens.

XX WO200234915-A2.

XX PD 02-MAY-2002.

XX PN WO200234915-A2.

XX PD 02-MAY-2002.

XX PF 25-OCT-2001; 2001WO-US42813.

XX PR 27-OCT-2000; 2000US-0697590.

XX PA (NYMO-) NYMOX PHARM CORP.

XX PI Fitzpatrick J, Averback P, Focht MSS, Bibiano R;

XX PS WPI; 2002-507998/54.

XX DR

XX New Haril peptide sequences of the Neural Thread Protein, useful in therapeutic assays, e.g. as targets for developing drugs for treating Alzheimer's disease, ischæmia or cerebral infarction, or for diagnosing these diseases

XX PS Claim 3; Page 29; 53PP; English.

XX The present invention describes a neural thread protein (NTP) peptide

CC having an amino acid sequence selected from ABB81511 to ABB81529 and their homologues, which are referred collectively as Haril peptides (I).

CC (I) have neuroprotective, nootropic, vasotropic and cerebroprotective activities, and can be used in peptide therapy. The Haril peptide

CC sequences can be used as analogues for NTP in therapeutic or diagnostic assays by replacing NTP with the peptide in such an assay. The Haril

CC peptides are also useful as a trap material in a diagnostic or therapeutic assay. Therefore, the Haril peptides are useful in binding

CC assays, protein and antibody purification, therapeutics or diagnostics. In particular, the peptides are also useful for diagnosing Alzheimer's

CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas, glioblastomas, hypoxia, ischæmia or cerebral infarction. The peptides

CC are also useful as targets for drug development for the treatment of these diseases. The present sequence represents a specifically claimed peptide from the present invention.

XX Sequence 13 AA;

Query Match 100.0%; Score 21; DB 23; Length 13;

Best Local Similarity 100.0%; Pred. No. 96; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 9 HARL 12

Query Match 100.0%; Score 21; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 89; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 2 HARL 5

RESULT 17

ABB81532
 ID ABB81532 standard; peptide; 13 AA.

XX ABB81532;
 AC
 XX

DT 02-SEP-2002 (first entry)

DE Neural thread protein (NTP) peptide #22.

XX Neural thread protein; NTP; Haril peptide; Alzheimer's disease;

KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;

KW hypoxia; ischaemia; cerebral infarction.

OS Homo sapiens.

XX WO200234915-A2.

XX PD 02-MAY-2002.

XX PN WO200234915-A2.

XX PD 02-MAY-2002.

XX PF 25-OCT-2001; 2001WO-US42813.

XX PR 27-OCT-2000; 2000US-0697590.

XX PA (NYMO-) NYMOX PHARM CORP.

XX PI Fitzpatrick J, Averback P, Focht MSS, Bibiano R;

XX DR

XX New Haril peptide sequences of the Neural Thread Protein, useful in therapeutic assays, e.g. as targets for developing drugs for treating Alzheimer's disease, ischæmia or cerebral infarction, or for diagnosing these diseases

XX PS Claim 3; Page 29; 53PP; English.

XX The present invention describes a neural thread protein (NTP) peptide

CC having an amino acid sequence selected from ABB81511 to ABB81529 and their homologues, which are referred collectively as Haril peptides (I).

CC (I) have neuroprotective, nootropic, vasotropic and cerebroprotective activities, and can be used in peptide therapy. The Haril peptide

CC sequences can be used as analogues for NTP in therapeutic or diagnostic assays by replacing NTP with the peptide in such an assay. The Haril

CC peptides are also useful as a trap material in a diagnostic or therapeutic assay. Therefore, the Haril peptides are useful in binding

CC assays, protein and antibody purification, therapeutics or diagnostics. In particular, the peptides are also useful for diagnosing Alzheimer's

CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas, glioblastomas, hypoxia, ischæmia or cerebral infarction. The peptides

CC are also useful as targets for drug development for the treatment of these diseases. The present sequence represents a specifically claimed peptide from the present invention.

XX Sequence 13 AA;

Query Match 100.0%; Score 21; DB 23; Length 13;

Best Local Similarity 100.0%; Pred. No. 96; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 9 HARL 12

RESULT 18
 XX
 AAM0412
 ID AAM0412 standard; Peptide; 14 AA.
 XX
 AC
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Human protein fragment SEQ ID NO: 960.
 XX
 KW Human; single nucleotide polymorphism; SNP; paternity test;
 forensic test; aberrant protein expression.
 XX
 OS Homo sapiens.
 XX
 PN WO2001515670-A2.
 PR 19-JUL-2001.
 PT XX
 PT 05-JAN-2001; 2001WO-US00322.
 PR XX
 PT 07-JAN-2000; 2000US-0174962.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach MD;
 DR DR N-PSDB; AAR89561.
 XX
 PT Isolated human polynucleotides containing single nucleotide polymorphisms, useful for the treatment and diagnosis of e.g. cancer, infection and diabetes.
 PT XX
 Disclosure: Page 388; 475PP; English.

XX
 CC The present invention relates to human nucleic acids containing single nucleotide polymorphisms (SNPs). These can be used in forensic and paternity tests, and to aid in the treatment of diseases associated with aberrant protein expression, including cancer, amyloidosis, diabetes, Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis, glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis, meningitis, muscular disorders, dementia, neurological diseases, tuberculous sclerosis, male infertility, hypercalcaemia, blood pressure disorders, osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or autoimmunity. The present sequence is a peptide encoded by a polymorphism-containing oligonucleotide fragment of the invention.
 CC
 XX
 SQ Sequence 14 AA:
 Query Match 100.0%; Score 21; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;
 OY 1 HARL 4
 ||||
 Db 5 HARL 8
 RESULT 20
 ID ABB81534
 ID ABB81534 standard; Peptide; 14 AA.
 XX
 AC ABB81534;
 XX
 DT 02-SEP-2002 (first entry)
 DE Neural thread protein (NTP) peptide #24.
 XX
 KW Neural thread protein; NTP; Harlil peptide; Alzheimer's disease; Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma; KW hypoxia; ischaemia; cerebral infarction.
 XX
 OS Homo sapiens.
 XX
 PN WO200234915-A2.
 XX
 PD 02-MAY-2002.
 XX
 PT 25-OCT-2001; 2001WO-US42813.
 XX
 PR 27-OCT-2000; 2000US-0697590.
 XX
 PA (NYMO-) NYMOX PHARM CORP.
 XX

RESULT 19
 XX
 AAM0444
 ID AAM0444 standard; Peptide; 14 AA.
 XX
 AC
 XX
 DT 01-OCT-2001 (first entry)
 XX
 DE Human protein fragment SEQ ID NO: 992.
 XX
 KW Human; single nucleotide polymorphism; SNP; paternity test; forensic test; aberrant protein expression.

PI Fitzpatrick J, Averback P, Focht MSS, Biblano R; DR XX
 PT New Haril peptide sequences of the Neural thread protein, useful in
 PT therapeutic assays, e.g. as targets for developing drugs for treating
 PT Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
 PT these diseases -
 XX
 PS Claim 3; Page 30; 53pp; English.
 XX
 CC The present invention describes a neural thread protein (NTP) peptide
 CC having an amino acid sequence selected from ABB01511 to ABB01529 and
 CC their homologues, which are referred collectively as Haril peptides (I).
 CC (I) have neuroprotective, nootropic, vasotrophic and cerebroprotective
 CC activities, and can be used in peptide therapy. The Haril peptide
 CC sequences can be used as analogues for NTP in therapeutic or diagnostic
 CC assays by replacing NTP with the peptide in such an assay. The Haril
 CC peptides are also useful as a trap material in a diagnostic or
 CC therapeutic assay. Therefore, the Haril peptides are useful in binding
 CC assays, protein and antibody purification, therapeutics or diagnostics
 CC In particular, the peptides are also useful for diagnosing Alzheimer's
 CC disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
 CC glioblastomas, hypoxia, ischemia or cerebral infarction. The peptides
 CC are also useful as targets for drug development for the treatment of
 CC these diseases. The present sequence represents a specifically claimed
 CC peptide from the present invention.
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 100.0%; Score 21; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps
 Qy 1 HARL 4
 XX AC AAY79924;
 Db 5 HARL 8
 XX
 DT 10-MAY-2000 (first entry)
 XX
 DE Human papillomavirus 16 E2 derived peptide M36A.
 XX
 KW Papillomavirus; PV; infection; cell proliferation; E2; peptidomimetic;
 KW EL; antiviral; viricide; cytostatic; anti-proliferative; dermatological;
 KW preneoplastic lesion; neoplastic lesion; cutaneous lesion; wart;
 KW epidermodysplasia verruciformis; anorectal carcinoma.
 XX
 OS Human papillomavirus.
 OS Synthetic.
 XX
 PN WO200001720-A2.
 XX
 PD 13-JAN-2000.
 XX
 PF 02-JUL-1999; 99WO-US13144.
 XX
 PR 02-JUL-1998; 98US-0091661.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Howley P, Benson J, Kasukawa H;
 XX
 DR WPI; 2000-171001/15.
 XX
 PT Use of papillomavirus E2 protein peptidomimetics for treating
 PT papillomavirus-infected cells and papillomavirus-induced conditions in
 XX

PT	mammals by inhibiting E1-E2 interaction	-
PS	Disclosure; Fig 10; 110pp; English.	
XX	The present invention describes the use of a small organic compound (A) which competitively inhibits interaction of a papillomavirus (PV) E2 protein with a PV E1 protein for treating a cell infected with PV or a mammal with a PV-induced condition. (A) has antiviral, virucide, cytotoxic, antiproliferative and dermatological activities. Methods from the present invention can be used to treat PV-induced conditions including growth of PV preneoplastic and neoplastic lesions, cutaneous lesions chosen from warts or other benign cutaneous lesions, Plantar warts (verruca plantaris), common warts (verruca plana), Butcher's common warts, flat warts, genital warts (condyloma acuminatum) and epidermodysplasia verruciformis, laryngeal, oral, pharyngeal, oesophageal and other upper airway papilloma or vaginal, cervical, vulvar, penile and anorectal carcinoma. The E2 inhibitors may also be used to treat epithelial and intestinal fibropapillomas in animals. The present sequence represents a peptide sequence used in the exemplification of the present invention.	
CC	XX	SQ
CC	Sequence 15 AA;	
CC	Query Match 100.0%; score 21; DB 21; Length 15;	
CC	Best Local Similarity 100.0%; Pred. No. 1.1e+02;	
CC	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CC	Qy 1 HARL 4	
CC	Db 3 HARL 6	
AC	RESULT 22	
AC	ABB81535 standard; peptide; 15 AA.	
AC	XX	
AC	ABB81535;	
AC	XX	
AC	DT 02-SEP-2002 (first entry)	
DE	XX	
DE	Neural thread protein (NTP) peptide #25.	
KW	XX	
KW	Neural thread protein; NTP; Haril peptide; Alzheimer's disease; Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma; hypoxia; ischaemia; cerebral infarction.	
KW	XX	
KW	Homo sapiens.	
OS	XX	
PN	PN WO200234915-A2.	
PD	XX	
PD	02-MAY-2002.	
XX	XX	
PF	PP 25-OCT-2001; 20001WO-US42813.	
XX	XX	
PR	PR 27-OCT-2000; 2000US-0697590.	
XX	XX	
PA	PA (NYMO-) NYMOX PHARM CORP.	
XX	XX	
PI	PI Fitzpatrick J, Averbach P, Rocht MSS, Bibiano R;	
XX	XX	
DR	DR WPI; 2002-507998/54.	
PS	PS Claim 3; Page 30; 53pp; English.	
XX	XX	
CC	The present invention describes a neural thread protein (NTP) peptide having an amino acid sequence selected from ABB81511 to ABB81529 and their homologues, which are referred collectively as Haril peptides (I). (I) have neuroprotective, nootropic, vasotropic and cerebroprotective	
CC	XX	
CC	PT New Haril peptide sequences of the Neural Thread Protein, useful in therapeutic assays, e.g. as targets for developing drugs for treating Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing these diseases -	
PT	XX	

activities, and can be used in peptide therapy. The Haril peptide sequences can be used as analogues for NTP in therapeutic or diagnostic assays by replacing NTP with the peptide in such an assay. The Haril peptides are also useful as a trap material in a diagnostic or therapeutic assay. Therefore, the Haril peptides are useful in binding assays, protein and antibody purification, therapeutics or diagnostics. In particular, the peptides are also useful for diagnosing Alzheimer's disease, Down's syndrome, neuroectodermal tumours, astrocytomas, glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides are also useful as targets for drug development for the treatment of these diseases. The present sequence represents a specifically claimed peptide from the present invention.

SQ Sequence 15 AA;

Query Match 100.0%; Score 21; DB 23; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 4;
Matches 0; Indels 0; Gaps 0;

Oy 1 HARL 4
Db 11 HARL 14

RESULT 23

ID ABB81530 standard; peptide; 16 AA.
XX ABB81530
AC
DT 02-SEP-2002 (first entry)

DE Neural thread protein (NTP) peptide #20.
XX
KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma; hypoxia; ischaemia; cerebral infarction.
OS Homo sapiens.
XX
PN WO200234915-A2.

XX
KW Neural thread protein; Haril Peptide; Alzheimer's disease; Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma; hypoxia; ischaemia; cerebral infarction.
OS Homo sapiens.
XX
PN 02-MAY-2002.

XX
PF 25-OCT-2001; 2001WO-US42813.
XX
PR 27-OCT-2000; 2000US-0697590.

XX
PA (NYMO-) NYMOX PHARM CORP.
XX
PI Fitzpatrick J, Averback P, Focht MSS, Bibiano R;
XX
DR WPI; 2002-507998/54.

XX
PT New Haril peptide sequences of the Neural Thread Protein, useful in therapeutic assays, e.g. as targets for developing drugs for treating Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing these diseases -

PS Claim 3; Page 29; 53pp; English.
The present invention describes a neural thread protein (NTP) peptide having an amino acid sequence selected from ABB81511 to ABB81529 and their homologues, which are referred collectively as Haril peptides (I). (I) have neuroprotective, nootropic, vasotrophic and cerebroprotective activities, and can be used in peptide therapy. The Haril peptide sequences can be used as analogues for NTP in therapeutic or diagnostic assays by replacing NTP with the peptide in such an assay. The Haril peptides are also useful as a trap material in a diagnostic or therapeutic assay. Therefore, the Haril peptides are useful in binding assays, protein and antibody purification, therapeutics or diagnostics. In particular, the peptides are also useful for diagnosing Alzheimer's disease, Down's syndrome, neuroectodermal tumours, astrocytomas,

CC glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides are also useful as targets for drug development for the treatment of these diseases. The present sequence represents a specifically claimed peptide from the present invention.

SQ Sequence 16 AA;

Query Match 100.0%; score 21; DB 23; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Mismatches 4;
Matches 0; Conservative 0; Indels 0; Gaps 0;

Oy 1 HARL 4
Db 2 HARL 5

RESULT 24

ID AAR80293 standard; protein; 17 AA.
XX AAR80293;
AC
DT 19-JAN-1996 (first entry)

DE Trehalose releasing enzyme internal fragment.

XX
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose; alpha-maltotetrasyltrehalose; alpha-maltotetrosyltrehalose; maltopentaosyltrehalose; sweetener; taste-improving agent; stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics; pharmaceuticals.
OS Rhizobium sp. M1.
XX
PN EP671470-A2.
XX
PD 13-SEP-1995.
XX
PF 07-MAR-1995; 95EP-0301474.
XX
PR 07-MAR-1994; 94JP-0059840.
XX
PR 07-MAR-1994; 94JP-0059834.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
XX
DR WPI; 1995-312772/41.
XX
PT DNA encoding a trehalose releasing enzyme - which releases trehalose from a non-reducing saccharide having a trehalose structure as an end unit.
XX
PS Example 2; Page 26; 45pp; English.

The trehalose releasing enzyme can be used for the preparation of trehalose with high yields and efficiency from non-reducing saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose, alpha-maltotetrasyltrehalose, alpha-maltotetrosyltrehalose and maltopentaosyltrehalose. The trehalose can be used as a sweetener, taste-improving agent, quality-improving agent, stabiliser, filler, excipient or adjuvant in food products, cosmetics and pharmaceuticals. This is an internal fragment of the enzyme.

SQ Sequence 17 AA;

Query Match 100.0%; Score 21; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Mismatches 4;
Matches 0; Conservative 0; Indels 0; Gaps 0;

Oy 1 HARL 4
Db 11 HARL 14

XX
XX WPI; 2000-038500/03.
XX DR
XX PT
PT Novel bacterial yjeQ polypeptides used to identify broad spectrum
XX antibiotics -
PS Claim 3; Fig 2d; 37pp; English.

CC
CC The present invention describes a novel family of polypeptides, CC
CC designated the yjeQ family. These polypeptides are required for the CC
growth of both gram negative and gram positive bacteria. The yjeQ CC
polypeptides and polynucleotides can be used in a method to identify CC
antagonists and antibacterial compounds. These antagonists and compounds CC
can be used to treat bacterial infections. New antibiotics are urgently CC
needed, as serious bacterial infections and antibiotic resistant strains CC
are becoming increasingly prevalent. The polypeptides of the invention CC
are essential proteins for bacterial viability, and represent new CC
targets for antibiotics. The present sequence represents a yjeQ family CC
member polypeptide sequence.
XX Sequence 30 AA;

Query Match 100 %; Score 21; DB 21; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 2 HARL 5

RESULT 28

AAU85095
ID AAU85095 standard; Peptide; 30 AA.

AC AAU85095;
XX DT 08-MAY-2002 (first entry)
DE Human PRAME segment 31.

XX KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
OS Homo sapiens.
XX WO200190197-A1.
XX PD 29-NOV-2001.
XX PF 25-MAY-2001; 2001WO-AU00622.
PR XX 26-MAY-2000; 2000AU-0007761.
PA (AUSU) UNIV AUSTRALIAN NAT.
PI Thomson SA, Ramshaw IA;
XX WPI; 2002-147575/19.
DR N-PSDB; ABK36915.

XX New synthetic polypeptides having several different segments of at
least one parent polypeptide linked together differently compared to
the linkage in the parent polypeptide, for inducing immune response
PT against a pathogen or cancer -
XX Example 3; Fig 27; 364pp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising
several different segments of at least one parent polypeptide linked
together in a different relationship relative to their linkage in the
XX

CC Parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for
CC designing the synthetic polypeptides. The synthetic polypeptides and
CC polynucleotides are referred to as a Savine. The synthetic polypeptide is
CC useful for modulating immune responses preferably directed against a
CC pathogen or a cancer, e.g., cancers of the lung, breast, ovary, cervix,
CC colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone
CC liver, oesophagus, brain, testicle, uterus), as potentiating agents.
Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Menningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella, Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present
CC sequence is a peptide derived from a parent protein used to
CC construct a savine of the invention.

SQ Sequence 30 AA;

Query Match 100.0%; Score 21; DB 23; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 16 HARL 19

RESULT 29

AAU85096
ID AAU85096 standard; Peptide; 30 AA.

AC AAU85096;
XX DT 08-MAY-2002 (first entry)
DE Human PRAME segment 32.

XX KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
OS Homo sapiens.
XX WO200190197-A1.
XX PD 29-NOV-2001.
XX PF 25-MAY-2001; 2001WO-AU00622.
PR XX 26-MAY-2000; 2000AU-0007761.
PA (AUSU) UNIV AUSTRALIAN NAT.
XX PI Thomson SA, Ramshaw IA;
XX WPI; 2002-147575/19.
DR N-PSDB; ABK36916.

XX New synthetic polypeptides having several different segments of at
least one parent polypeptide linked together differently compared to
the linkage in the parent polypeptide, for inducing immune response
PT against a pathogen or cancer -
XX Example 3; Fig 27; 364pp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising
several different segments of at least one parent polypeptide linked
together in a different relationship relative to their linkage in the
XX

CC together in a different relationship relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide or for inducing an immune response against a pathogen or cancer. Also included are a synthetic polynucleotide encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polynucleotides are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone, liver, oesophagus, brain, testicle, uterus), as potentiating agents. Compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human immunodeficiency virus), hepatitis, influenza, Japanese encephalitis virus, Epstein-Barr virus and respiratory syncytial virus, bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, CC trypanosoma, Toxoplasma and Giardia) infections. The present sequence is a peptide derived from a parent protein used to construct a savine of the invention.

XX Sequence 30 AA;

Query Match 100.0%; Score 21; DB 23; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 1 HARL 4

RESULT 30

AAW94447 standard, peptide; 31 AA.
ID AAW94447;
XX AC ;
XX DT 15-APR-1999 (first entry)

DE Mutant proproricin linker region for MMP-11, PAP-284.
XX Ricin-like toxin; cancer; viral infection; parasitic infection; KW linker; B chain; A chain; protease; fungal infection; malaria; leucocyte proliferation; cytomegalovirus; herpes; hepatitis; rhinovirus; laryngotracheitis; poliomyleitis; varicella zoster; KW cystic fibrosis; multiple sclerosis.
OS Unidentified.
OS Synthetic.

PN W09849311-A2.
XX DD 05-NOV-1998.
XX PF 30-APR-1998; 98WO-CA00394.
XX PR 29-OCT-1997; 97US-0063715.
XX PR 30-APR-1997; 97US-0045148.
(DNOV-) DE NOVO ENZYME CORP.
PI Borgford T;
XX DR WPI; 1999-009431/01.

XX New nucleic acid encoding ricin-like toxin with an interchain linker cleaved by protease - is specific for diseased cells, useful for, e.g. killing selectively cancer or infected cells

PS Claim 24; FIG 41D; 352pp; English.
XX

CC The present invention describes new purified and isolated nucleic acids (I) encoding: (i) the A and B chains of a ricin-like toxin (II); and (ii) a heterologous linker, joining the two chains and including a cleavage recognition site for a disease-specific protease (III). Also described are: (1) plasmids or baculovirus transfer vectors that contain (I); and (2) recombinant protein (IV) consisting of the A and B chains of (II) joined by the specified linker. (IV) produced by expression of (I) in host cells, are used to inhibit or kill diseased cells that produce (III), particularly for treating cancers (e.g. leucocyte proliferation; cancer of ovary, pancreas, breast or prostate; glioma) or infections caused by fungi, parasites (e.g. malaria) or viruses (e.g. cytomegalovirus (CMV), herpes, hepatitis, rhinovirus, laryngotracheitis, poliomyelitis or varicella zoster, also cystic fibrosis and multiple sclerosis. Alternatively, (I) is used to express (IV) in vivo. (IV) is toxic specifically for (III)-expressing cells and does not defend for specificity on a cell-binding component. When used to treat virus-infected cells, transcytosis and cytotoxicity of (IV) are increased by retrograde translocation from endoplasmic reticulum to cytoplasm (which some viruses exploit to avoid immune detection), so selectivity and safety are further improved. (IV) are not toxic until chain A is released and this occurs only in target cells. The present sequence represents a specifically claimed mutant proproricin linker from the present invention.

XX Sequence 31 AA;

Query Match 100.0%; Score 21; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 20 HARL 23

RESULT 31

AAB34676 standard; Protein; 32 AA.
ID AAB34676
XX AC ;
XX DT 26-JAN-2001 (first entry)

XX Human secreted protein sequence encoded by gene 44 SEQ ID NO:160.
XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; KW antirheumatic; antiproliferative; cytostatic; cardiotonic; vasotropic; KW cerebroprotective; nootropic; neuroprotective; antibiotic; virucide; KW fungicide; opthalmological; gene therapy; autoimmune disease; neoplasm; KW hyperproliferative disorder; cancer; cardiovascular disorder; infection; KW cerebrovascular disorder; angiogenesis; nervous system disorder; infection; KW ocular disorder; wound healing; skin aging; food additive; preservative; KW Homo sapiens.
XX OS WO20056751-A1.
XX PN WO20056751-A1.
XX PD 28-SEP-2000.
XX PR 09-MAR-2000; 2000WO-US06013.
XX PR 19-MAR-1999; 99US-0125360.
XX PR 11-JUN-1999; 99US-0138626.
XX PR 03-DEC-1999; 99US-0168662.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Ruben SM, Komatsoulis G;
XX DR WPI; 2000-579482/54.
XX PT Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition

XX
PS Disclosure; Page 413; 419pp; English.
 XX
 CC The polynucleotide sequences given in AAC59738 to AAC59787 encode the
 CC human secreted proteins given in AAB34577 to AAB34626. AAB34627 to
 CC ABB4686 represent human secreted polypeptide sequences and proteins
 homologous to them, which are given in the exemplification of the present
 invention. Human secreted proteins have activities based on the tissues
 and cells the genes are expressed in. Example of activities include:
 CC cytostatic; cardiotonic; vasotropic; cerebroprotective; nootropic;
 CC neuroprotective; antibacterial; virucide; fungicide; and
 CC ophthalmological. The polynucleotides and proteins can be used to
 prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 rabbits, goats, horses, cats, dogs, chickens or sheep. They are also
 used in diagnosing a pathological condition or susceptibility to a
 pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases, hyperproliferative disorders e.g. neoplasms and
 CC cancers of the breast or liver, cardiovascular disorders,
 CC cerebrovascular disorders, angiogenesis, nervous system disorders,
 CC infections caused by bacteria, viruses and fungi and ocular disorders.
 CC The proteins can also be used to aid wound healing and epithelial cell
 proliferation to prevent skin aging due to sunburn, to maintain organs
 before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues and in chemotaxis. The proteins can also be used
 as a food additive or preservative to increase or decrease storage
 capabilities. AAC59729 to AAC59737 and AAB34576 represent sequences used
 CC in the exemplification of the present invention.

XX Sequence 32 AA;

Query Match	100.0%	Score	21	DB	21	Length	32
Best Local Similarity	100.0%	Pred. No.	2.4e+02				
Matches	4	Conservative	0	Mismatches	0	Indels	0
Qy	1 HARL 4			Ov			
Db	10 HARL 13						

RESULT 32

ID	ABB31475	ABB31475 standard; Peptide; 32 AA.
AC	ABB31475;	
XX		
DT	01-FEB-2002 (first entry)	
DE	Peptide #4126 encoded by breast cell single exon nucleic acid probe.	
KW	Human; microarray; single exon probe; gene expression; breast; disease; cancer.	
XX		
OS	Homo sapiens.	
XX		
PN	WO20015271-A2.	
XX		
PD	09-AUG-2001.	
XX		
PF	30-JAN-2001; 2001WO-US00662.	
XX		
PR	04-FEB-2000; 2000US-0180312.	
PR	26-MAY-2000; 2000US-0207456.	
PR	30-JUN-2000; 2000US-0608408.	
PR	03-AUG-2000; 2000US-0632366.	
PR	21-SEP-2000; 2000US-0234667.	
PR	27-SEP-2000; 2000US-0236359.	
PR	04-OCT-2000; 2000US-0242463.	
XX		
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
XX		
PI	Penn SG, Hanzel DK, Chen W, Rank DR;	
XX		

DR WPI; 2001-496933/54.

XX
 PT New spatially-addressable set of single exon nucleic acid probes,
 PR useful for measuring gene expression in sample derived from human
 breast, comprises number of single exon nucleic acid probes -
 XX
 PS Claim 27; SEQ ID NO 14443; 327pp + sequence listing; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting
 CC the probes with a collection of detectably labelled nucleic acids
 CC derived from mRNA of human breast, and then measuring the label
 CC bound to each probe of the microarray. The probes are useful for
 CC verifying the expression of regions of genomic DNA predicted to
 CC encode proteins. They are useful for gene discovery and for
 CC determining predisposition and/or prognosis breast disease. Gene
 CC expression analysis is useful for assessing the toxicity of chemical
 CC agents on cells. The microarray of this invention presents a far greater
 CC diversity of probes for measuring gene expression, with far less bias
 than expressed sequence tag microarrays. The method is suitable for
 CC rapid production of functional information from genomic sequence. The
 CC present sequence is a peptide encoded by a single exon nucleic acid
 CC probe of the invention. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp://wipo.int/pub/published_pct_sequences.

XX Sequence 32 AA;

Query Match	100.0%	Score	21	DB	22	Length	32
Best Local Similarity	100.0%	Pred. No.	2.4e+02				
Matches	4	Conservative	0	Mismatches	0	Indels	0
Qy	1 HARL 4			Ov			
Db	12 HARL 15						

RESULT 33

ID	ABB36687	ABB36687 standard; Peptide; 32 AA..
AC	ABB36687;	
XX		
DT	04-FEB-2002 (first entry)	
DE	Peptide #4193 encoded by human foetal liver single exon probe.	
KW	Human; foetal liver; gene expression; single exon nucleic acid probe.	
XX		
OS	Homo sapiens.	
XX		
PN	WO20015277-A2.	
XX		
PD	09-AUG-2001.	
XX		
PR	30-JAN-2001; 2001WO-US00669.	
XX		
PR	04-FEB-2000; 2000US-0180312.	
PR	26-MAY-2000; 2000US-0207456.	
PR	30-JUN-2000; 2000US-0608408.	
PR	03-AUG-2000; 2000US-0632366.	
PR	21-SEP-2000; 2000US-0234667.	
PR	27-SEP-2000; 2000US-0236359.	
PR	04-OCT-2000; 2000US-0242463.	
XX		
PA	(MOLE-) MOLECULAR DYNAMICS INC.	
XX		
PI	Penn SG, Hanzel DK, Chen W, Rank DR;	
XX		

PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
 XX
 PS Claim 27; SEQ ID NO 29322; 630pp + sequence listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 32 AA;
 XX
 Query Match 100 %; Score 21; DB 22; Length 32;
 Best Local Similarity 100 %; Pred. No. 2.4e-02; Mismatches 0; Indels 0; Gaps 0
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 Qy 1 HARL 4
 Db 12 HARL 15
 XX
 RESULT 34
 ABB2024 ID ABB2024 standard; Protein; 32 AA.
 XX
 AC ABB2024;
 XX
 DT 23-JAN-2002 (first entry)
 DE Protein #4023 encoded by probe for measuring heart cell gene expression.
 XX Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 OS Homo sapiens.
 XX WO20015274-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00666.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-48899/53.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human hearts -
 XX
 PS Claim 15; SEQ ID NO 23794; 530pp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,

CC diagnosing, grading, staging, monitoring and prognosis diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
 Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published-pct-sequences](http://wipo.int/pub/published-pct-sequences).

QY 1 HARL 4
|||
Db 12 HARL 15

RESULT 36

ARM69846
ID AAM69846 standard; Protein; 32 AA.
XX
AC ARM69846;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30152.
XX
KW Human; bone marrow; expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
WO200157276-A2.

XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PR Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI: 2001-488901/53.

XX
PT Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 27: SEQ ID NO 22294; 487PP; English.

XX
CC The present invention relates to human single exon nucleic acid probes
(SENP; see AAI10068 AAI28459). The present sequence is a peptide encoded
by one such probe. The SENPs are derived from human HeLa cells. The SENPs
can be used to produce a single exon microarray, which can be used for
measuring human gene expression in a sample derived from human cervical
epithelial cells. By measuring gene expression, the probes are therefore
useful in grading and/or staging of diseases of the cervix, notably
cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 32 AA;

Query Match	100.0%	Score 21;	DB 22;	Length 32;
Best Local Similarity	100.0%	Pred. No. 2.4e+02;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 HARL 4
|||
Db 12 HARL 15

RESULT 37

AAM17668
ID AAM17668 standard; Protein; 32 AA.
XX
AC AAM17668;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #4222 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.

XX
PR 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.

XX
PD 09-AUG-2001.
XX
PR 30-JAN-2001; 2001WO-US00670.

XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0508408.
PR 03-AUG-2000; 2000US-0532366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.

XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PR Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI: 2001-488901/53.

XX
PT Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 27: SEQ ID NO 22294; 487PP; English.

XX
CC The present invention relates to human single exon nucleic acid probes
(SENP; see AAI10068 AAI28459). The present sequence is a peptide encoded
by one such probe. The SENPs are derived from human HeLa cells. The SENPs
can be used to produce a single exon microarray, which can be used for
measuring human gene expression in a sample derived from human cervical
epithelial cells. By measuring gene expression, the probes are therefore
useful in grading and/or staging of diseases of the cervix, notably
cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 32 AA;

Query Match	100.0%	Score 21;	DB 22;	Length 32;
Best Local Similarity	100.0%	Pred. No. 2.4e+02;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 HARL 4
|||
Db 12 HARL 15

RESULT 38

AAM30185
ID AAM30185 standard; Protein; 32 AA.
XX
AC AAM30185;
XX
DT 17-OCT-2001 (first entry)
XX
DE Peptide #4222 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.

XX
PR 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00663.

xx
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-020756.
 PR 30-JUN-2000; 2000US-0508408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234887.
 PR 21-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-488897/53.
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human Placenta -
 XX PS Claim 27; SEQ ID NO 30454; 654pp; English.
 XX The present invention relates to single exon nucleic acid probes (SENPs:
 CC see AI13115-AA157546). The present sequence is a peptide encoded by one
 such probe. The probes are useful for producing a microarray for
 predicting, measuring and displaying gene expression in samples derived
 CC from human Placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.
 XX SQ sequence 32 AA:
 Query Match 100.0%; Score 21; DB 22; Length 32;. Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 DB 12 HARL 15
 RESULT 39
 AAM05331 ID . AAM05331 standard; protein; 32 AA.
 AC AAM05331;
 XX DT 09-OCT-2001 (first entry)
 DE Peptide #4013 encoded by probe for measuring breast gene expression.
 XX Probe; human; breast disease; breast cancer; development disorder;
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 XX OS Homo sapiens.
 XX PN WO200157270-A2.
 XX PD 09-AUG-2001.
 XX PF 29-JAN-2001; 2001WO-US00661.
 XX PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-476286/51.
 XX
 PT Novel single exon nucleic acid probe used to measuring gene expression
 PT in a human breast -
 XX
 PR Claim 27; SEQ ID NO 14071; 32pp; English.
 XX
 CC The present invention relates to novel single exon nucleic acid probes
 CC (see AI100010-AA11067). The present sequence is a peptide encoded by one
 such probe. The probes are useful for measuring human gene expression in
 a human breast sample, where the probe hybridises at high stringency to a
 nucleic acid expressed in the human breast. The probes are useful for
 predicting, diagnosing, grading, staging, monitoring and prognosis
 diseases of the human breast, particularly those diseases with polygenic
 aetiology. The diseases include; breast cancer, disorders of development,
 inflammatory diseases of the breast, fibrocytic changes, proliferative
 breast disease and non-carcinoma tumours.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_pct-sequences.
 XX SQ Sequence 32 AA:
 Query Match 100.0%; Score 21; DB 22; Length 32;. Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 DB 12 HARL 15
 RESULT 40
 AGB39474 ID AGB39474 standard; Peptide; 32 AA.
 AC AGB39474;
 XX DT 19-AUG-2002 (first entry)
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 29139.
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangiomyomatosis; Kartagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX OS Homo sapiens.
 XX PN WO200186003-A2.
 XX PD 15-NOV-2001.
 XX PF 30-JAN-2001; 2001WO-US00665.
 XX PR 04-FEB-2000; 2000US-180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-0508408P.
 PR 03-AUG-2000; 2000US-0632366P.
 PR 21-SEP-2000; 2000US-234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-0024263P.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2002-114183/15.
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to

PT measure gene expression in human lung samples -
 XX
 PS Claim 27; SEQ ID No 29139; 634pp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frame (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemostasis, pulmonary histiocytosis, lymphangiomyomatosis, pulmonary alveolar proteinosis, Kartagener syndrome, fibrocytic and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention.
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 21; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db 12 HARL 15
 RESULT 41
 AAO09129 ID AAO09129 standard; Protein: 36 AA.
 AC AAO09129;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 23021.
 XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 OS Homo sapiens.
 XX PN WO200164835-A2.
 XX PD 07-SEP-2001.
 XX PR 26-FEB-2001; 2001WO-US04927.
 XX PR 28-FEB-2000; 2000US-051126.
 XX PR 18-MAY-2000; 2000US-0577409.
 PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT;
 XX DR WPI; 2001-51438/56.
 DR N-PDB; AAI89060.
 PT Isolated nucleic acids and polypeptides, useful for preventing PT diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
 XX PS Claim 20; SEQ ID NO 23021; 1399pp + Sequence Listing; English.
 XX CC The invention relates to human polynucleotides (AAI7941-AAI93811) and the encoded proteins (AAU00010-AAU0310) that exhibit activity relating to cytokine cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The vaccines or polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
 CC Note: The sequence data for this Patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
 XX SQ Sequence 36 AA;
 Query Match 100.0%; Score 21; DB 22; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db 13 HARL 16
 RESULT 42
 AAO08247 ID AAO08247 standard; Protein: 37 AA.
 AC AAO08247;
 XX DE 06-Nov-2001 (first entry)
 XX Human polypeptide SEQ ID NO 22139.
 XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 OS Homo sapiens.
 XX PN WO200164835-A2.
 XX PD 07-SEP-2001.
 XX PR 26-FEB-2001; 2001WO-US04927.
 XX PR 28-FEB-2000; 2000US-051126.
 PR 18-MAY-2000; 2000US-0577409.

XX	PA	07-JUL-2000;	2000US-0216880.
XX	PR	11-JUL-2000;	2000US-0217487.
PT	PR	14-JUL-2000;	2000US-0218290.
XX	PR	14-AUG-2000;	2000US-0220963.
DR	PR	26-JUL-2000;	2000US-0220964.
N-PSDB; AA188178.	PR	14-AUG-2000;	2000US-0224519.
XX	PT	14-AUG-2000;	2000US-0224519.
XX	PT	14-AUG-2000;	2000US-0225213.
XX	PT	14-AUG-2000;	2000US-0225214.
XX	PT	14-AUG-2000;	2000US-0225266.
PS	PS	14-AUG-2000;	2000US-0225267.
XX	PS	14-AUG-2000;	2000US-0225268.
XX	PS	14-AUG-2000;	2000US-0225270.
CC	CC	14-AUG-2000;	2000US-0225447.
CC	CC	14-AUG-2000;	2000US-0225757.
CC	CC	14-AUG-2000;	2000US-0225758.
CC	CC	14-AUG-2000;	2000US-0225759.
CC	CC	14-AUG-2000;	2000US-0226279.
CC	CC	14-AUG-2000;	2000US-0226681.
CC	CC	22-AUG-2000;	2000US-0226680.
CC	CC	22-AUG-2000;	2000US-0227182.
CC	CC	22-AUG-2000;	2000US-0227209.
CC	CC	23-AUG-2000;	2000US-0228241.
CC	CC	30-AUG-2000;	2000US-0228242.
CC	CC	01-SEP-2000;	2000US-0229407.
CC	CC	01-SEP-2000;	2000US-0229345.
CC	CC	01-SEP-2000;	2000US-0229513.
XX	SQ	05-SEP-2000;	2000US-0230437.
XX	Sequence	37 AA;	
RESULT 43	Query Match	100.0%;	score 21; DB 22; length 37;
AAM9435	Best Local Similarity	100.0%;	Pred. No. 2.7e+0;
ID AAM9435	Matches	4;	Mismatches 0;
XX	AC	Indels	0;
XX	AC	Gaps	0;
XX	AC		
AAM94835;	XX		
XX	DT	21-NOV-2001 (first entry)	
DE	Human reproductive system related antigen	SEQ ID NO: 3493.	
XX	XX		
OS Homo sapiens.	XX		
PN WO20155320-A2.	XX		
XX	PD	02-AUG-2001.	
XX	PP	17-JAN-2001; 20001WO-US01339.	
XX	PR	31-JAN-2000; 20000US-017905.	
PR	04-FEB-2000; 20000US-0180628.		
PR	24-FEB-2000; 20000US-0184664.		
PR	02-MAR-2000; 20000US-0186350.		
PR	16-MAR-2000; 20000US-0189874.		
PR	17-MAR-2000; 20000US-0190076.		
PR	18-APR-2000; 20000US-019823.		
PR	19-MAY-2000; 20000US-020515.		
PR	07-JUN-2000; 20000US-0209467.		
PR	30-JUN-2000; 20000US-0214886.		
PR	07-JUL-2000; 20000US-0216647.		

AAU20929		PR	08-SEP-2000; 20000US-0231413.
ID AAU20929	standard; Protein; 43 AA.	PR	08-SEP-2000; 20000US-0231414.
XX		PR	08-SEP-2000; 20000US-0232080.
AC		PR	08-SEP-2000; 20000US-0232081.
XX		PR	12-SEP-2000; 20000US-0231988.
DT	18-DEC-2001 (first entry)	PR	14-SEP-2000; 20000US-0233997.
XX	Human novel foetal antigen, SEQ ID NO 1173.	PR	14-SEP-2000; 20000US-0232398.
DE		PR	14-SEP-2000; 20000US-0232199.
XX		PR	14-SEP-2000; 20000US-0232401.
KW	Human; foetal tissue antigen; antiinflammatory; neuroprotective;	PR	14-SEP-2000; 20000US-02331063.
KW	immunomodulator; cardiovascular; cytostatic; nephrotoxic;	PR	14-SEP-2000; 20000US-0233064.
KW	cardiovascular; autoimmune disease; rheumatoid arthritis;	PR	14-SEP-2000; 20000US-0233065.
KW	hyperproliferative disorder; breast neoplasm; cancer;	PR	14-SEP-2000; 20000US-0234223.
KW	cardiovascular disorder; cardiac arrest; cerebrovascular disorder;	PR	21-SEP-2000; 20000US-0234274.
KW	cerebral ischaemia; angiogenesis; nervous system disorder;	PR	25-SEP-2000; 20000US-0234997.
KW	Alzheimer's disease; infection; ocular disorder; corneal infection;	PR	25-SEP-2000; 20000US-0234998.
KW	wound healing; epithelial cell proliferation; food additive.	PR	26-SEP-2000; 20000US-0235494.
XX		PR	27-SEP-2000; 20000US-0235834.
OS	Homo sapiens.	PR	27-SEP-2000; 20000US-0235836.
XX		PR	29-SEP-2000; 20000US-0236327.
PN	WO200155312-A2.	PR	29-SEP-2000; 20000US-0236367.
XX		PR	29-SEP-2000; 20000US-0236368.
PD	02-AUG-2001.	PR	29-SEP-2000; 20000US-0236359.
XX		PR	29-SEP-2000; 20000US-0236370.
PF	17-JAN-2001; 2001WO-US01321.	PR	PR 02-OCT-2000; 20000US-0236802.
PR	31-JAN-2000; 20000US-0179065.	PR	02-OCT-2000; 20000US-0227037.
PR	04-FEB-2000; 20000US-0180028.	PR	02-OCT-2000; 20000US-02377038.
PR	24-FEB-2000; 20000US-0184664.	PR	02-OCT-2000; 20000US-02377039.
PR	02-MAR-2000; 20000US-0186350.	PR	02-OCT-2000; 20000US-02377040.
PR	16-MAR-2000; 20000US-0189874.	PR	13-OCT-2000; 20000US-0239935.
PR	17-MAR-2000; 20000US-0190076.	PR	13-OCT-2000; 20000US-0239937.
PR	18-APR-2000; 20000US-0198123.	PR	20-OCT-2000; 20000US-0240960.
PR	19-MAY-2000; 20000US-0205515.	PR	20-OCT-2000; 20000US-0241221.
PR	07-JUN-2000; 20000US-0209467.	PR	20-OCT-2000; 20000US-0241785.
PR	28-JUN-2000; 20000US-0214886.	PR	20-OCT-2000; 20000US-0241787.
PR	07-JUL-2000; 20000US-0215135.	PR	20-OCT-2000; 20000US-0241808.
PR	07-JUL-2000; 20000US-0216647.	PR	20-OCT-2000; 20000US-0241809.
PR	11-JUL-2000; 20000US-0217787.	PR	20-OCT-2000; 20000US-0241826.
PR	11-JUL-2000; 20000US-0217496.	PR	01-NOV-2000; 20000US-0244617.
PR	14-JUL-2000; 20000US-0218290.	PR	08-NOV-2000; 20000US-0245474.
PR	26-JUL-2000; 20000US-0220963.	PR	08-NOV-2000; 20000US-0246475.
PR	14-AUG-2000; 20000US-0220664.	PR	08-NOV-2000; 20000US-0246476.
PR	14-AUG-2000; 20000US-0224518.	PR	08-NOV-2000; 20000US-0246477.
PR	14-AUG-2000; 20000US-0224519.	PR	08-NOV-2000; 20000US-0246478.
PR	14-AUG-2000; 20000US-0225213.	PR	08-NOV-2000; 20000US-0246523.
PR	14-AUG-2000; 20000US-0225214.	PR	08-NOV-2000; 20000US-0246524.
PR	14-AUG-2000; 20000US-0225266.	PR	08-NOV-2000; 20000US-0246525.
PR	14-AUG-2000; 20000US-0225267.	PR	08-NOV-2000; 20000US-0246526.
PR	14-AUG-2000; 20000US-0225268.	PR	08-NOV-2000; 20000US-0246527.
PR	14-AUG-2000; 20000US-0226279.	PR	08-NOV-2000; 20000US-0246528.
PR	22-AUG-2000; 20000US-0226681.	PR	08-NOV-2000; 20000US-0246532.
PR	14-AUG-2000; 20000US-0225447.	PR	08-NOV-2000; 20000US-0246533.
PR	14-AUG-2000; 20000US-0225757.	PR	08-NOV-2000; 20000US-0246534.
PR	14-AUG-2000; 20000US-0225758.	PR	08-NOV-2000; 20000US-0246535.
PR	14-AUG-2000; 20000US-0225759.	PR	08-NOV-2000; 20000US-0246536.
PR	18-AUG-2000; 20000US-0226279.	PR	08-NOV-2000; 20000US-0246537.
PR	22-AUG-2000; 20000US-0226681.	PR	08-NOV-2000; 20000US-0246538.
PR	22-AUG-2000; 20000US-022688.	PR	08-NOV-2000; 20000US-0246539.
PR	01-SEP-2000; 20000US-0227182.	PR	08-NOV-2000; 20000US-0246540.
PR	05-SEP-2000; 20000US-0227009.	PR	08-NOV-2000; 20000US-0246541.
PR	30-AUG-2000; 20000US-0228924.	PR	08-NOV-2000; 20000US-0246542.
PR	01-SEP-2000; 20000US-0229287.	PR	08-NOV-2000; 20000US-0246543.
PR	06-SEP-2000; 20000US-0229343.	PR	08-NOV-2000; 20000US-0246544.
PR	01-SEP-2000; 20000US-0229344.	PR	17-NOV-2000; 20000US-0249207.
PR	01-SEP-2000; 20000US-0229345.	PR	17-NOV-2000; 20000US-0249208.
PR	05-SEP-2000; 20000US-0229509.	PR	17-NOV-2000; 20000US-0249210.
PR	05-SEP-2000; 20000US-0229513.	PR	17-NOV-2000; 20000US-0249211.
PR	06-SEP-2000; 20000US-0230437.	PR	17-NOV-2000; 20000US-0249212.
PR	06-SEP-2000; 20000US-0230438.	PR	17-NOV-2000; 20000US-0249213.
PR	08-SEP-2000; 20000US-0231242.	PR	17-NOV-2000; 20000US-0249214.
PR	08-SEP-2000; 20000US-0231243.	PR	17-NOV-2000; 20000US-0249215.
PR	08-SEP-2000; 20000US-0231244.	PR	17-NOV-2000; 20000US-0249216.
PR	17-NOV-2000; 20000US-0249245.	PR	17-NOV-2000; 20000US-0249246.
PR	17-NOV-2000; 20000US-0249265.	PR	17-NOV-2000; 20000US-0249266.

PR 07-JAN-2000; 2000US-0174847.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis G;
 XX DR
 XX WPI; 2000-611720/58.

XX
 PT New nucleic acid molecules encoding 45 human secreted proteins for
 XX diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -
 XX
 PS Disclosure; Page 385; 410pp; English.

XX
 The invention relates to the isolation of genes AAC93310-C93354 encoding
 CC new nucleic acid molecules encoding 45 human secreted proteins for
 CC diagnosing, preventing, treating or ameliorating medical conditions and
 CC used as food additives or preservatives -
 XX
 PS Disclosure; Page 386; 410pp; English.

XX
 The invention relates to the isolation of genes AAC93310-C93354 encoding
 CC the human secreted proteins AAB11380-B51423. The genes and proteins are
 CC useful for preventing, ameliorating or treating medical conditions, e.g.
 CC by protein or gene therapy. The genes are isolated from a range of human
 CC tissues disclosed in the specification. The nucleic acids, proteins,
 CC and (anti)agonists are useful in the diagnosis, treatment and
 prevention of: (a) cancer, e.g. breast and ovarian cancer, and other
 CC cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital, (b) immune disorders
 CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections. The present sequence is a protein isolated in the
 CC present invention.

XX
 Sequence 47 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	21	47
Matches	100.0%	Pred. No. 3.5e+02;	
Db	0	Mismatches	0;
Qy	1 HARL 4	Indels	0;
Db	38 HARL 41	Gaps	0;

RESULT 48
 AAB51460
 ID AAB51460 standard; Protein; 47 AA.
 XX
 AC AAB51460;
 XX DT 16-FEB-2001 (first entry)
 DE Human secreted protein BLAST search protein SEQ ID NO: 137.
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW antiallergic; hepatotropic; antidiabetic; antifungal; antiparasitic;
 KW cardiotonic; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein.
 OS Homo sapiens.
 XX PN WO200058195-A1.
 XX PD 05-OCT-2000.
 XX PR 23-MAR-2000; 2000WO-US07661.
 XX PR 26-MAR-1999; 99US-0126504.
 XX PR 07-JAN-2000; 2000US 0174847.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM, Komatsoulis G;
 XX DR WPI; 2000-619225/59.

XX
 WPI; 2000-611720/58.
 XX
 The invention relates to the isolation of genes AAC93310-C93354 encoding
 CC the human secreted proteins AAB11380-B51423. The genes and proteins are
 CC useful for preventing, ameliorating or treating medical conditions, e.g.
 CC by protein or gene therapy. The genes are isolated from a range of human
 CC tissues disclosed in the specification. The nucleic acids, proteins,
 CC and (anti)agonists are useful in the diagnosis, treatment and
 prevention of: (a) cancer, e.g. breast and ovarian cancer, and other
 CC cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital, (b) immune disorders
 CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections. The present sequence is a protein isolated in the
 CC present invention.

XX
 Sequence 47 AA;

Query Match	Score	DB	Length
Best Local Similarity	100.0%	21	47
Matches	100.0%	Pred. No. 3.5e+02;	
Db	0	Mismatches	0;
Qy	1 HARL 4	Indels	0;
Db	38 HARL 41	Gaps	0;

RESULT 49
 AAB51688
 ID AAB51688 standard; Protein; 47 AA.
 XX
 AC AAB51688;
 XX DT 26-FEB-2001 (first entry)
 XX DE Human secreted protein sequence encoded by gene 23 SEQ ID NO:128.
 KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
 KW antirheumatic; antiproliferative; cytostatic; cardiotonic; vasotropics;
 KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; gene therapy; autoimmune disease; infection;
 KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;
 KW cerebrovascular disorder; nervous system disorder; ocular disorder;
 KW wound healing; skin aging; food additive; preservative.
 OS Homo sapiens.
 XX PN WO200061620-A1.
 XX PD 19-OCT-2000.
 XX PF 06-APR-2000; 2000WO-US09069.
 XX PR 09-APR-1999; 99US-0128702.
 XX PR 20-JAN-2000; 2000US-0177049.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PA (ROSE/) ROSEN C A.
 XX PI Rosen CA, Ruben SM, Komatsoulis G;
 XX DR WPI; 2000-619225/59.

XX
PT Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition -

XX
PT Disclosure; Page 504; 540pp; English.
The polynucleotide sequences given in AAC93364 to AAC93412 encode the human secreted proteins given in AAB51620 to AAB51668. AAB51669 to AAB51722 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include:

CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiotropic; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and ophthalmological; antidiabetic; fungicide; and prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases, hyperproliferative disorders, cardiovascular disorders, cerebrovascular disorders, angiogenesis, nervous system disorders, infections caused by bacteria, viruses and fungi and ocular disorders. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organ before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities AAC93355 to AAC93363 and AAC93169 represent sequences which are used in the exemplification of the present invention.

XX Sequence 47 AA;
Query Match 100.0%; Score 21; DB 21; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; QY 1 HARL 4
Db 38 HARL 41

DR WPI; 2001-514838/56.
DR N-PSPB; AA191410.

XX PT Isolated nucleic acids and polypeptides, useful for preventing and diagnosing and treating e.g. leukaemia, inflammation and immune disorders -

XX PS Claim 20; SEQ ID NO 25371; 1399pp + Sequence Listing; English.
The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA00010-AA013910) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct-sequences](http://wipo.int/pub/published/pct-sequences).

XX SQ Sequence 47 AA;

Query Match 100.0%; Score 21; DB 22; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; QY 1 HARL 4
Db 37 HARL 40

Search completed: November 13, 2002, 13:41:00
Job time : 37 secs

RESULT 50
AA011479
ID AA011479 standard; Protein: 47 AA.
XX AC AA011479;
XX DT 06-NOV-2001 (first entry)
DE Human polypeptide SEQ ID NO 25371.

XX Human polypeptide SEQ ID NO 25371.
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PR 26-FEB-2001; 2001WO-US04927.
XX PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YP, Liu C, Drmanac RT;
XX

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OM protein - protein search, using sw model

Run on: November 13, 2002, 13:39:28 ; Search time 16 Seconds
 (without alignments)
 24.034 Million cell updates/sec

Searcher:	Scorer:	Score:	Length:	DB:	Query:
US-09-697-590-2_COPY_292_295	HARL 4	21	45	2	283224
BLOSUM62					
Gapext 0.5					

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	21	100	0	hypothetical protein B97644
2	21	100	0	hypothetical protein B69101
3	21	100	0	hypothetical protein S28481
4	21	100	0	hypothetical protein AR2590
5	21	100	0	hypothetical protein B69337
6	21	100	0	hypothetical protein C70501
7	21	100	0	chlorophyll a/b binding protein T06193
8	21	100	0	hypothetical protein F82684
9	21	100	0	hypothetical protein G84144
10	21	100	0	hypothetical protein H97404
11	21	100	0	hypothetical protein AH2622
12	21	100	0	hypothetical protein E83358
13	21	100	0	hypothetical protein T20227
14	21	100	0	hypothetical protein S38916
15	21	100	0	hypothetical protein A97833
16	21	100	0	hypothetical protein C81012
17	21	100	0	hypothetical protein A9744
18	21	100	0	hypothetical protein A12701
19	21	100	0	hypothetical protein D97412
20	21	100	0	hypothetical protein S04786
21	21	100	0	hypothetical protein JQ0389
22	21	100	0	hypothetical protein T07540
23	21	100	0	hypothetical protein S43154
24	21	100	0	hypothetical protein QOCVBL
25	21	100	0	hypothetical protein D49339
26	21	100	0	hypothetical protein I18
27	21	100	0	hypothetical protein 157506
28	21	100	0	hypothetical protein 177386
29	21	100	0	hypothetical protein E70718

ALIGMENTS

Query	Match	Best Local Similarity	Score	DB	Length
RESULT 1	B97644	100.0%	21	DB 2	44
		Best Local Similarity	100.0%	Pred. No.	69;
		Matches	4;	Mismatches	0;
		QY	1 HARL 4	Indels	0;
		Db	12 HARL 15	Gaps	0;

RESULTS

Result	No.	Score	Length	DB	ID	Description
1	1	21	44	2	B97644	hypothetical protein B97644
2	2	21	59	2	B69101	hypothetical protein B69101
3	3	21	65	2	S28481	hypothetical protein S28481
4	4	21	67	2	AR2590	hypothetical protein AR2590
5	5	21	71	2	B69337	hypothetical protein B69337
6	6	21	74	2	C70501	hypothetical protein C70501
7	7	21	100	0	T06193	chlorophyll a/b binding protein T06193
8	8	21	100	0	F82684	hypothetical protein F82684
9	9	21	100	0	G84144	hypothetical protein G84144
10	10	21	100	0	H97404	hypothetical protein H97404
11	11	21	100	0	AH2622	hypothetical protein AH2622
12	12	21	100	0	E83358	hypothetical protein E83358
13	13	21	100	0	T20227	hypothetical protein T20227
14	14	21	100	0	S38916	hypothetical protein S38916
15	15	21	100	0	A97833	hypothetical protein A97833
16	16	21	100	0	C81012	hypothetical protein C81012
17	17	21	100	0	A9744	hypothetical protein A9744
18	18	21	100	0	A12701	hypothetical protein A12701
19	19	21	100	0	D97412	hypothetical protein D97412
20	20	21	100	0	S04786	hypothetical protein S04786
21	21	21	100	0	JQ0389	hypothetical protein JQ0389
22	22	21	100	0	T07540	hypothetical protein T07540
23	23	21	100	0	S43154	hypothetical protein S43154
24	24	21	100	0	QOCVBL	hypothetical protein QOCVBL
25	25	21	100	0	D49339	hypothetical protein D49339
26	26	21	100	0	I18	hypothetical protein I18
27	27	21	100	0	157506	hypothetical protein 157506
28	28	21	100	0	177386	hypothetical protein 177386
29	29	21	100	0	E70718	hypothetical protein E70718

Query Match Best Local Similarity 100.0% ; Score 21; DB 2; Length 59;
 Pred. No. 93;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Db 15 HARL 18

RESULT 3

rfbQ protein - *Vibrio cholerae* (strain O17)
 C;Species: *Vibrio cholerae*
 C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999
 C;Accession: S28481
 R;Manning, P.A.
 submitted to the EMBL Data Library, May 1991
 A;Reference number: S28467
 A;Molecule type: DNA
 A;Accession: S28481
 A;Residues: 1-65 <MAN>
 A;Cross-references: EMBL:X59554; NID:948381; PIDN:CAA42147.1; PID:948396
 A;Experimental source: strain O17
 C;Genetics:
 A;Gene: rfbQ

Query Match 100.0%; Score 21; DB 2; Length 65;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 53 HARL 56

RESULT 4

hypothetical protein Attu0115 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: *Agrobacterium tumefaciens*
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C;Accession: AF2590
 R;Wood, D.W.; Setubal, C.J.; Kauh, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Gillet, W.; Grant, J.; Guenther, D.; Kutayav, T.; Levy, R.; Li, M.; McClellan, R.; Karp, P.; Romero, P.; Zhang, S.; Science, 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Steer, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; PMID:11743193
 A;Accession: AF2590
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-67 <KUR>
 A;Experimental source: strain C58 (DuPont)
 C;Genetics:
 A;Gene: Attu0115
 A;Map position: circular chromosome.

Query Match 100.0%; Score 21; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 53 HARL 56

RESULT 5

hypothetical protein AF0698 - *Archaeoglobus fulgidus*
 C;Species: *Archaeoglobus fulgidus*
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C;Accession: B69337

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.P.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodds, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Nature 390, 364-370, 1997
 A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaean *Archaeoglobus fulgidus*
 A;Reference number: A69250; NID:98049343; PMID:9389475
 A;Accession: B69337
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-71 <KLE>
 A;Cross-references: GB:AE001056; GB:AE000782; NID:92689379; PIDN:AA0546.1; PID:9264
 A;Accession: B69337
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-71 <KLE>
 A;Cross-references: GB:AE001056; GB:AE000782; NID:92689379; PIDN:AA0546.1; PID:9264
 A;Accession: B69337
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-71 <KLE>
 A;Cross-references: GB:AE001056; GB:AE000782; NID:92689379; PIDN:AA0546.1; PID:9264
 A;Accession: B69337
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-71 <KOL>
 A;Cross-references: GB:Z98266; GB:AL123456; NID:93261839; PIDN:CAB10941.1; PID:e33277
 A;Experimental source: strain H37Rv
 C;Genetics:
 A;Gene: Rv1684

Query Match 100.0%; Score 21; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 61 HARL 64

RESULT 6

hypothetical protein Rv1684 - *Mycobacterium tuberculosis* (strain H37Rv)
 C;Species: *Mycobacterium tuberculosis*
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C;Accession: C70501
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, R.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genomic sequence
 A;Reference number: A70500; NID:9829587; PMID:9634230
 A;Accession: C70501
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-74 <COL>
 A;Cross-references: GB:Z98266; GB:AL123456; NID:93261839; PIDN:CAB10941.1; PID:e33277
 A;Experimental source: strain H37Rv
 C;Genetics:
 A;Gene: Rv1684

Query Match 100.0%; Score 21; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 61 HARL 64

RESULT 7

chlorophyll a/b-binding protein - barley (fragment)
 C;Species: *Hordeum vulgare* (Barley)
 C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000
 C;Accession: T06193
 R;Humbbeck, K.; Krupinska, K.
 submitted to the EMBL Data Library, May 1998
 A;Description: Differential regulation of chlorophyll a/b-binding proteins and ELIP j
 A;Reference number: Z15522
 A;Accession: T06193
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-75 <HUM>
 A;Cross-references: EMBL:AJ006296; PIDN:CAA06961.1
 A;Experimental source: cv. Carina, leaf
 C;Genetics:
 A;Gene: CP29
 C;Superfamily: chlorophyll a/b-binding protein

C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosystem II; thylakoid

Query Match 100.0%; Score 21; DB 2; Length 83;

Best Local Similarity 100.0%; **Pred.** No. 1.3e+02; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Matches 4; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 HARL 4
|||
Db 30 HARL 33

RESULT 8

F82684 hypothetical protein XFL1417 [imported] - *Xylella fastidiosa* (strain 9a5c)

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: F82684

R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequer

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: A82515; MURID:20365717; PMID:1010347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: F82684

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-80 <ST>

A;Cross-references: GB:AE003972; GB:AE003849; NID:9106418; PIDN:AAF84226.1; GSPDB:GN001

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Almeida, M.R.S.; Bueno, M.R.P.; Camargo, A.N.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H.; CesNeto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

J.; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froehlich, D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laiggi M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaak M.; Tshukao, M.H.; Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silveira, R.C.; Palmieri, D.A.; Authors: da Silva, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.; Gene: XFL1417

Query Match 100.0%; Score 21; DB 2; Length 80;

Best Local Similarity 100.0%; **Pred.** No. 1.3e+02; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Matches 4; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 HARL 4
|||
Db 53 HARL 56

RESULT 9

G84144 hypothetical protein BH3959 [imported] - *Bacillus halodurans* (strain C-125)

C;Species: *Bacillus halodurans*

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C;Accession: G84144

R;Takami, H.; Nakane, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirano, Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and

A;Reference number: A83650; MURID:20512582; PMID:11058132

A;Accession: G84144

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-83 <ST>

A;Cross-references: GB:AP001520; GB:BA000004; NID:910176401; PIDN:BAB07678.1; GSPDB:GN00

A;Experimental source: strain C-125

C;Genetics: C;Genetics:

A;Gene: BH3959

Query Match 100.0%; Score 21; DB 2; Length 83;

Best Local Similarity 100.0%; **Pred.** No. 1.3e+02; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Matches 4; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 HARL 4
|||
Db 7 HARL 10

RESULT 10

H97404 hypothetical protein AGC_C_659 [imported] - *Agrobacterium tumefaciens* (strain C58, C;Species: *Agrobacterium tumefaciens*

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002

C;Accession: H97404

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quroollo, B.; Golz, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium*

A;Reference number: A97359; PMID:11743194

A;Accession: H97404

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-85 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK86193.1; PID:915155290; GSPDB:GN00169

A;Gene: AGC_C_659

A;Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 85;

Best Local Similarity 100.0%; **Pred.** No. 1.4e+02; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Matches 4; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 HARL 4
|||
Db 7 HARL 10

RESULT 11

AH2622 conserved hypothetical protein Atu0376 [imported] - *Agrobacterium tumefaciens* (stra

C;Species: *Agrobacterium tumefaciens*

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

C;Accession: AH2622

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; McC erge, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McC ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Koster, E.W.

A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A;Reference number: AB2577; PMID:11743193

A;Accession: AH2622

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-85 <KUR>

A;Cross-references: GB:AE008688; PIDN:AAI41398.1; PID:917738716; GSPDB:GN00186

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: Atu0376

A;Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 85;

Best Local Similarity 100.0%; **Pred.** No. 1.4e+02; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Matches 4; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 HARL 4
|||
Db 7 HARL 10

RESULT 12

E83358

hypothetical protein PA2292 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: E83358
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Harbig, K.; Lin, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-93 <STO>
 A;Cross-references: GB:AE004655; GB:AE004091; NID:99948321; PIDN:AAG05680.1; GSPDB:GN001
 A;Experimental source: strain PA01
 C;Genetics:
 A;Gene: PA2292

Query Match 1 HARL 4
 |||||
 Db 31 HARL 34

RESULT 13
 hypothetical protein C54G10.1 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C;Accession: T20227
 R;Matthews, L.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: 219240
 A;Accession: T20227
 A;Status: Preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-93 <WIL>
 A;Cross-references: EMBL:275532; PIDN:CA99809.1; GSPDB:GN00023; CBSP:C54G10.1
 A;Experimental source: clone C54G10
 C;Genetics:
 A;Gene: CESP:C54G10.1
 A;Map position: 5

Query Match 1 HARL 4
 |||||
 Db 31 HARL 34

RESULT 14
 hypothetical protein 4 - phage phi-C31
 C;Species: Phage phi-C31
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999
 C;Accession: S38916
 R;Hartley, N.M.; Murphy, G.O.; Bruton, C.J.; Chater, K.F.
 submitted to the EMBL Data Library, November 1993
 A;Reference number: S38912
 A;Accession: S38916
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-96 <HAR>
 A;Cross-references: EMBL:X76288; NID:9432610; PIDN:CA53915.1; PID:9432615
 Query Match 1 HARL 4
 |||||
 Best Local Similarity 100.0%; Score 21; DB 2; Length 96;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 HARL 4
 |||||
 Db 82 HARL 85

RESULT 15
 hypothetical protein RC1065 [imported] - *Rickettsia conorii* (strain Malish 7)
 C;Species: *Rickettsia conorii*
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
 C;Accession: A97833
 R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Science 293, 2093-2098, 2001
 A;Title: Mechanisms of Evolution in *Rickettsia conorii* and *Rickettsia prowazekii*.
 A;Reference number: A97700; MUID:21442074; PMID:11557893
 A;Accession: A97833
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-100 <KUR>
 A;Cross-references: GB:AE006914; PIDN:ALA03603.1; PID:915620185; GSPDB:GN00173
 C;Genetics:
 A;Gene: RC1065

Query Match 1 HARL 4
 |||||
 Db 77 HARL 80

RESULT 16
 conserved hypothetical protein NMB2058 [imported] - *Neisseria meningitidis* (strain MC)
 C;Species: *Neisseria meningitidis*
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
 C;Accession: C81012; G81953
 R;Tettelein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, B.; Hickey, E.K.; Haff, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.; Hori, H.; Olin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.; Science 287, 1809-1815; 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappoport, R.; A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755; PMID:10710307
 A;Accession: C81012
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-101 <TET>
 A;Cross-references: GB:AE002555; GB:AE002098; NID:97227310; PIDN:AAFA2378.1; PID:9724
 A;Experimental source: serogroup B, strain MC58
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; McRory, S.; Jarrels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491
 A;Reference number: A81775; MUID:20222556; PMID:10761919
 A;Accession: G81953
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-101 <PAR>
 A;Cross-references: GB:AL162753; GB:AL157959; NID:9739120; PIDN:CA803678.1; PID:9739
 A;Experimental source: serogroup A, strain Z2491
 C;Genetics:
 A;Gene: NMB2058; NMDA001

Query Match 1 HARL 4
 |||||
 Best Local Similarity 100.0%; Score 21; DB 2; Length 101;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 HARL 15

RESULT 17

A;Title: Genomic Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

C;Species: Agrobacterium tumefaciens

C;Accession: A97484

A;Reference number: A97359; PMID:11743194

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-103 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK86253.1; PID:915155361; GSPDB:GN00169

A;Genetics:

A;Gene: AGR_C_774

A;Map position: circular chromosome

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A;Reference number: A97359; PMID:11743194

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-103 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK86253.1; PID:915155361; GSPDB:GN00169

A;Genetics:

A;Gene: AGR_C_1876

A;Map position: circular chromosome

A;Title: Genomic Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A;Reference number: A97359; PMID:11743194

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-103 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK86253.1; PID:915155361; GSPDB:GN00169

A;Genetics:

A;Gene: AGR_C_1876

A;Map position: circular chromosome

A;Title: Genomic Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A;Reference number: A97359; PMID:11743194

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-103 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK86253.1; PID:915155361; GSPDB:GN00169

A;Genetics:

A;Gene: AGR_C_1876

A;Map position: circular chromosome

A;Title: Genomic Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A;Reference number: A97359; PMID:11743194

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-103 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK86253.1; PID:915155361; GSPDB:GN00169

A;Genetics:

A;Gene: AGR_C_1876

A;Map position: circular chromosome

A;Title: Genomic Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A;Reference number: A97359; PMID:11743194

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-103 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK86253.1; PID:915155361; GSPDB:GN00169

A;Genetics:

A;Gene: AGR_C_1876

A;Map position: circular chromosome

A;Title: Genomic Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A;Reference number: A97359; PMID:11743194

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-103 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK86253.1; PID:915155361; GSPDB:GN00169

A;Genetics:

A;Gene: AGR_C_1876

A;Map position: circular chromosome

A;Title: Genomic Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens

A;Reference number: A97359; PMID:11743194

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-103 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK86253.1; PID:915155361; GSPDB:GN00169

A;Genetics:

A;Gene: AGR_C_1876

A;Map position: circular chromosome

Science 294, 2323-2328, 2001.

A;Title: Genomic Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A;Reference number: A97359; PMID:11743194

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-103 <KUR>

A;Cross-references: GB:AE007869; PIDN:AAK86253.1; PID:915155361; GSPDB:GN00169

A;Genetics:

A;Gene: AGR_C_774

A;Map position: circular chromosome

Query Match 100.0%; Score 21; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 61 HARL 64

Query Match 100.0%; Score 21; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 45 HARL 48

Query Match 100.0%; Score 21; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 11 HARL 14

Query Match 100.0%; Score 21; DB 2; Length 106;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 11 HARL 14

Query Match 100.0%; Score 21; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 11 HARL 14

Query Match 100.0%; Score 21; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 11 HARL 14

Query Match 100.0%; Score 21; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 11 HARL 14

Query Match 100.0%; Score 21; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 11 HARL 14

Query Match 100.0%; Score 21; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 11 HARL 14

Query Match 100.0%; Score 21; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 11 HARL 14

Query Match 100.0%; Score 21; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 11 HARL 14

Query Match 100.0%; Score 21; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 11 HARL 14

Query Match 100.0%; Score 21; DB 2; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4 ||||| Db 11 HARL 14

A;Species: Homo sapiens (man)	C;Date: 02-Jul-1996	#sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I57506	C;Date: 24-Aug-2001	#sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
R;Coulter, F.; Kumar, R.; Ernst, M.; Klein, R.; Martin-Zanca, D.; Barbacid, M.	R;Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; He	Proc. Natl. Acad. Sci. U.S.A. 98: 9899-9894, 2001
Mol. Cell. Biol. 10, 4202-4210, 1990	Qy 1 HARL 4	A;Title: The complete sequence of the 1,693-kb PSYMB megaplasmid from the N2-fixing
A;Reference number: 157506; MUID:90310386; PMID:1695324	Db 7 HARL 10	A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: 157506	Oy 1 HARL 4	A;Status: preliminary
A;Cross-references: GB:M55336; NID:g339913; PIDN:AAA36768.1; PID:g339914	Db 96 HARL 99	A;Molecule type: mRNA
A;Residues: 1-118 <RES>	Oy 1 HARL 4	A;Genetics:
A;Gene: trk2	Db 96 HARL 99	
RESULT 27	Query Match 100.0%; Score 21; DB 2; Length 118;	Score 21; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;	Best Local Similarity 100.0%; Pred. No. 1.9e+02;	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 HARL 4	Qy 1 HARL 4	
Db 7 HARL 10	Db 7 HARL 10	
A;Species: Sinorhizobium meliloti	C;Species: Sinorhizobium meliloti	
oncogene tyrosine Protein kinase receptor - human (fragment)	C;Species: Homo sapiens (man)	
C;Accession: 177386	C;Accession: C96008	
C;Date: 02-Aug-1996	C;Date: 24-Aug-2001	#sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: I77386	R;Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; He	Proc. Natl. Acad. Sci. U.S.A. 98: 9899-9894, 2001
Mol. Cell. Biol. 10, 4202-4210, 1990	Qy 1 HARL 4	A;Title: The complete sequence of the 1,693-kb PSYMB megaplasmid from the N2-fixing
A;Title: Human trk oncogenes activated by point mutation, in-frame deletion, and duplication	Db 7 HARL 10	A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: 177386	Oy 1 HARL 4	A;Accession: C96008
A;Status: preliminary; translated from GB/EMBL/DBJ	Db 7 HARL 10	A;Status: preliminary
A;Molecule type: mRNA	Oy 1 HARL 4	A;Molecule type: DNA
A;Residues: 1-118 <RES>	Db 7 HARL 10	A;Residues: 1-120 <KRB>
A;Cross-references: GB:M55337; NID:g339915; PIDN:AAA36769.1; PID:g339916	Oy 1 HARL 4	A;Cross-references: GB:AL591985; PIDN:CAC49731.1; PID:g15141218; GSPDB:GN00167
A;Genetics:	Db 7 HARL 10	A;Experimental source: strain 1021, megaplasmid pSYMB
A;Gene: trk4	Oy 1 HARL 4	R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barley-Hult
Query Match 100.0%; Score 21; DB 2; Length 118;	Db 7 HARL 10	pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
Best Local Similarity 100.0%; Pred. No. 1.9e+02;	Oy 1 HARL 4	L.; Hyman, R.W.; Jones, T.
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db 7 HARL 10	Science 293: 668-672, 2001
Qy 1 HARL 4	Oy 1 HARL 4	A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Leja
Db 7 HARL 10	Db 7 HARL 10	hebuilt, P.; Vandembroucq, M.; Vorholtter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
RESULT 28	Query Match 100.0%; Score 21; DB 2; Length 120;	A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
RT0718	Best Local Similarity 100.0%; Pred. No. 1.9e+02;	A;Reference number: A96039; MUID:21368234; PMID:11474104
hypothetical protein Rv0967 - Mycobacterium tuberculosis (strain H37Rv)	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Contents: annotation
C;Species: Mycobacterium tuberculosis	Qy 1 HARL 4	C;Genetics:
C;Date: 17-Jul-1998	Db 7 HARL 10	A;Gene: SMM21501
#sequence_revision 17-Jul-1998 #text_change 22-Oct-1999	Oy 1 HARL 4	A;Genome: plasmid
C;Accession: E70118	Db 7 HARL 10	
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.	Query Match 100.0%; Score 21; DB 2; Length 120;	
i; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.	Best Local Similarity 100.0%; Pred. No. 1.9e+02;	
ReJandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Nature 393, 537-544, 1998	Qy 1 HARL 4	
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.	Db 7 HARL 10	
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome	Oy 1 HARL 4	
A;Reference number: A70500; MUID:98295987; PMID:9634230	Db 7 HARL 10	
A;Accession: E70118	Oy 1 HARL 4	
A;Status: preliminary; nucleic acid sequence not shown; translation not shown	Db 7 HARL 10	
A;Molecule type: DNA	Oy 1 HARL 4	
A;Residues: 1-119 <COL>	Db 7 HARL 10	
A;Cross-references: GB:279700; GB:AL123456; NID:g33261628; PIDN:CAB02009.1; PID:e1300050;	Oy 1 HARL 4	
A;Experimental source: strain H37Rv	Db 7 HARL 10	
A;Genetics:	Oy 1 HARL 4	
A;Gene: rplR	Db 7 HARL 10	
C;Superfamily: Escherichia coli ribosomal protein L18	Oy 1 HARL 4	
Query Match 100.0%; Score 21; DB 2; Length 121;	Db 7 HARL 10	
Best Local Similarity 100.0%; Pred. No. 1.9e+02;	Oy 1 HARL 4	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db 7 HARL 10	
Qy 1 HARL 4	Oy 1 HARL 4	
RESULT 29	Query Match 100.0%; Score 21; DB 2; Length 119;	
C96008	Best Local Similarity 100.0%; Pred. No. 1.9e+02;	
hypothetical membrane protein [imported] - Sinorhizobium meliloti (strain 1021) mage	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
C;Species: Sinorhizobium meliloti	Qy 1 HARL 4	
C;Accession: C96008	Db 96 HARL 99	
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; He	Oy 1 HARL 4	
Proc. Natl. Acad. Sci. U.S.A. 98: 9899-9894, 2001	Db 96 HARL 99	
A;Title: The complete sequence of the 1,693-kb PSYMB megaplasmid from the N2-fixing	Oy 1 HARL 4	
A;Reference number: A95842; MUID:21396508; PMID:11481431	Db 96 HARL 99	
A;Accession: C96008	Oy 1 HARL 4	
A;Status: preliminary	Db 96 HARL 99	
A;Molecule type: DNA	Oy 1 HARL 4	
A;Residues: 1-120 <KRB>	Db 96 HARL 99	
A;Cross-references: GB:AL591985; PIDN:CAC49731.1; PID:g15141218; GSPDB:GN00167	Oy 1 HARL 4	
A;Experimental source: strain 1021, megaplasmid pSYMB	Db 96 HARL 99	
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barley-Hult	Oy 1 HARL 4	
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.	Db 96 HARL 99	
L.; Hyman, R.W.; Jones, T.	Oy 1 HARL 4	
Science 293: 668-672, 2001	Db 96 HARL 99	
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Leja	Oy 1 HARL 4	
hebuilt, P.; Vandembroucq, M.; Vorholtter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,	Db 96 HARL 99	
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.	Oy 1 HARL 4	
A;Reference number: A96039; MUID:21368234; PMID:11474104	Db 96 HARL 99	
A;Contents: annotation	Oy 1 HARL 4	
C;Genetics:	Db 96 HARL 99	
A;Gene: SMM21501	Oy 1 HARL 4	
A;Genome: plasmid	Db 96 HARL 99	
RESULT 30	Query Match 100.0%; Score 21; DB 2; Length 120;	
E87139	Best Local Similarity 100.0%; Pred. No. 1.9e+02;	
50S ribosomal protein L18 [imported] - Mycobacterium leprae	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
C;Species: Mycobacterium leprae	Qy 1 HARL 4	
C;Accession: E87139	Db 84 HARL 87	
R;Cole, S.T.; Englemeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.	Oy 1 HARL 4	
R.; Davies, R.M.; Devin, R.K.; Duthoy, S.; Feitwell, T.; Fraser, A.; Hamlin, N.; Holl	Db 84 HARL 87	
eam, M.A.; Rutledge, K.M.	Oy 1 HARL 4	
Nature 409, 1007-1011, 2001	Db 84 HARL 87	
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.	Oy 1 HARL 4	
A;Title: Massive gene decay in the leprosy bacillus.	Db 84 HARL 87	
A;Reference number: A86909; MUID:21128732; PMID:11244002	Oy 1 HARL 4	
A;Accession: E87139	Db 84 HARL 87	
A;Status: preliminary	Oy 1 HARL 4	
A;Molecule type: DNA	Db 84 HARL 87	
A;Residues: 1-121 <STO>	Oy 1 HARL 4	
A;Cross-references: GB:AL450380; NID:g13093539; PIDN:CAC30797.1; GSPDB:GN00147	Db 84 HARL 87	
C;Genetics:	Oy 1 HARL 4	
A;Gene: rplR	Db 84 HARL 87	
C;Superfamily: Escherichia coli ribosomal protein L18	Oy 1 HARL 4	
Query Match 100.0%; Score 21; DB 2; Length 121;	Db 84 HARL 87	
Best Local Similarity 100.0%; Pred. No. 1.9e+02;	Oy 1 HARL 4	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db 84 HARL 87	
Qy 1 HARL 4	Oy 1 HARL 4	
RESULT 31	Query Match 100.0%; Score 21; DB 2; Length 120;	
E87139	Best Local Similarity 100.0%; Pred. No. 1.9e+02;	
50S ribosomal protein L18 [imported] - Mycobacterium leprae	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
C;Species: Mycobacterium leprae	Qy 1 HARL 4	
C;Accession: E87139	Db 84 HARL 87	
R;Cole, S.T.; Englemeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.	Oy 1 HARL 4	
R.; Davies, R.M.; Devin, R.K.; Duthoy, S.; Feitwell, T.; Fraser, A.; Hamlin, N.; Holl	Db 84 HARL 87	
eam, M.A.; Rutledge, K.M.	Oy 1 HARL 4	
Nature 409, 1007-1011, 2001	Db 84 HARL 87	
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.	Oy 1 HARL 4	
A;Title: Massive gene decay in the leprosy bacillus.	Db 84 HARL 87	
A;Reference number: A86909; MUID:21128732; PMID:11244002	Oy 1 HARL 4	
A;Accession: E87139	Db 84 HARL 87	
A;Status: preliminary	Oy 1 HARL 4	
A;Molecule type: DNA	Db 84 HARL 87	
A;Residues: 1-121 <STO>	Oy 1 HARL 4	
A;Cross-references: GB:AL450380; NID:g13093539; PIDN:CAC30797.1; GSPDB:GN00147	Db 84 HARL 87	
C;Genetics:	Oy 1 HARL 4	
A;Gene: rplR	Db 84 HARL 87	
C;Superfamily: Escherichia coli ribosomal protein L18	Oy 1 HARL 4	
Query Match 100.0%; Score 21; DB 2; Length 121;	Db 84 HARL 87	
Best Local Similarity 100.0%; Pred. No. 1.9e+02;	Oy 1 HARL 4	
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db 84 HARL 87	
Qy 1 HARL 4	Oy 1 HARL 4	

QY 1 HARL 4
 ||||
 Db 16 HARL 19

RESULT 31
 T37737
 hypothetical protein SPAC167.06c - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: *Schizosaccharomyces pombe*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
 C;Accession: T37737; T38952
 R;Rieger, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, January 1999
 A;Reference number: Z21743
 A;Accession: T37737
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-121 <RTS>
 A;Cross-references: EMBL:AL035248; PIDN:CAA22851.1; GSPDB:GN00066; SPDB:SPAC167.06c
 A;Experimental source: strain 972h-; cosmid C57A7
 R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, May 1997
 A;Reference number: Z21819
 A;Accession: T38952
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-121 <SKES>
 A;Cross-references: EMBL:Z95396; PIDN:CA08760.1; GSPDB:GN00056; SPDB:SPAC57A7.02c
 A;Experimental source: strain 972h-; cosmid C57A7
 C;Genetics:
 A;Gene: SPAC57A7.02c; SPAC167.06c
 A;Map position: 1

Query Match 100.0%; Score 21; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 ||||
 Db 35 HARL 38

RESULT 32
 T45382
 ribosomal protein L18 [imported] - *Mycobacterium leprae*
 C;Species: *Mycobacterium leprae*
 C;Accession: T45382
 C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 18-Feb-2000
 R;Cole, S.T.; Flisselles, B.; Honore, N.
 submitted to the EMBL Data Library, August 1997
 A;Reference number: Z22966
 A;Accession: T45382
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-122 <COL>
 A;Cross-references: EMBL:Z98756; PIDN:CAB11452.1
 A;Experimental source: cosmid B2492
 C;Genetics:
 A;Note: rplR
 C;Superfamily: *Escherichia coli* ribosomal protein L18
 Query Match 100.0%; Score 21; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 ||||
 Db 17 HARL 20

RESULT 33
 G81198

RESULT 34
 C81775
 hypothetical protein NMA2047 [imported] - *Neisseria meningitidis* (strain 22491 serogroup A)
 C;Species: *Neisseria meningitidis*
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C;Accession: C81775
 R;Pirkhill, J.; Achiman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; McHale, S.; Jagels, K.; Leather, S.R.; Moulis, S.; Mungall, K.; Quail, M.A.; Rajandream, M.; Holroyd, S.; Nature 404, 502-505, 2000
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491
 A;Reference number: A81775; MID:2022356; PMID:10761919
 A;Accession: C81775
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-122 <PAR>
 A;Cross-references: GB:AL162758; GB:AL157959; NIDB:g7380672; PIDN:CAB85265.1; PID:97366
 A;Experimental source: serogroup A, strain 22491
 C;Genetics:
 A;Gene: NMA2047

Query Match 100.0%; Score 21; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HARL 4
 ||||
 Db 76 HARL 79

RESULT 35
 D85843
 unknown protein encoded within prophage CP-933V [imported] - *Escherichia coli* (strain 22491 serogroup A)
 C;Species: *Escherichia coli*
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C;Accession: D85843
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mau, B.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.R.; Tettelein, H.; Saunders, N.J.; Heidelberg, J.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappoport, V.; Masignani, V.; Pizza, M.; Olin, H.; Vanathavan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Rieger, H.; Rajandream, M.A.; Barrell, B.G.; Churcher, C.M.; McLean, K.; Quail, M.A.; Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappoport, V.; Masignani, V.; Eisen, J.R.; Tettelein, H.; Saunders, N.J.; Heidelberg, J.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappoport, V.; Masignani, V.; Rieger, H.; Rajandream, M.A.; Barrell, B.G.; Churcher, C.M.; McLean, K.; Quail, M.A.; Science 287, 1809-1815, 2000
 A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58
 A;Reference number: A81000; MID:20175755; PMID:10710307
 A;Accession: G81198
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-122 <TET>
 A;Cross-references: GB:AE002400; GB:AE002098; NID:97225659; PIDN:AAF40876.1; PID:97225659
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB0438

A; Cross-references: GB:AE005174; NID:912516372; PIDN:AGS57208.1; GSPDB:GN00145; UWGP:233
 A; Experimental source: strain 0157:H7, substrain EDU933
 C; Genetics:
 A; Gene: Z3320

Query Match	100.0%	Score 21;	DB 2;	Length 124;
Best Local Similarity	100.0%	Pred. No.	2e+02;	
Matches	4;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY 1 HARL 4
 Db 104 HARL 107

RESULT 36

D85630 probable tail assembly chaperon [imported] - Escherichia coli (strain 0157:H7, substrain EDU933)

C; Species: Escherichia coli
 C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
 C; Accession: D85630
 R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca, Nature 409, 529-533, 2001
 A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
 A; Reference number: A85480; MUID:21074935; PMID:11206551
 A; Accession: D85630
 A; Status: preliminary
 A; Residues: 1-124 <STOC>
 A; Cross-references: GB:AER005174; NID:912514215; PIDN:AA655504.1; GSPDB:GN00145; UWGP:213
 C; Genetics:
 A; Gene: Z1371

Query Match	100.0%	Score 21;	DB 2;	Length 124;
Best Local Similarity	100.0%	Pred. No.	2e+02;	
Matches	4;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY 1 HARL 4
 Db 104 HARL 107

RESULT 37

F90822 probable tail assembly chaperone [imported] - Escherichia coli (strain 0157:H7, substrain EDU933)

C; Species: Escherichia coli
 C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C; Accession: F90822
 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H., DNA Res. 8, 11-22, 2001
 A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and reference number: A99629; MUID:21156231; PMID:11258796
 A; Accession: B90909
 A; Status: preliminary
 A; Residues: 1-124 <HAY>
 A; Cross-references: GB:BA000007; PIDN:BAB35665.1; PID:913361708; GSPDB:GN00154
 A; Experimental source: strain 0157:H7, substrain RIMD 0509952
 A; Gene: BCS2242

Query Match	100.0%	Score 21;	DB 2;	Length 124;
Best Local Similarity	100.0%	Pred. No.	2e+02;	
Matches	4;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY 1 HARL 4
 Db 104 HARL 107

RESULT 39

B90909 probable tail assembly chaperone [imported] - Escherichia coli (strain 0157:H7, substrain EDU933)

C; Species: Escherichia coli
 C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C; Accession: B90909
 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H., DNA Res. 8, 11-22, 2001
 A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and reference number: A99629; MUID:21156231; PMID:11258796
 A; Accession: B90909
 A; Status: preliminary
 A; Residues: 1-124 <HAY>
 A; Cross-references: GB:BA000007; PIDN:BAB35665.1; PID:913361708; GSPDB:GN00154
 A; Experimental source: strain 0157:H7, substrain RIMD 0509952
 A; Gene: BCS2242

Query Match	100.0%	Score 21;	DB 2;	Length 124;
Best Local Similarity	100.0%	Pred. No.	2e+02;	
Matches	4;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY 1 HARL 4
 Db 104 HARL 107

RESULT 40

E90876 probable tail assembly chaperone [imported] - Escherichia coli (strain 0157:H7, substrain EDU933)

C; Species: Escherichia coli
 C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
 C; Accession: E90876
 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H., DNA Res. 8, 11-22, 2001
 A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and reference number: A99629; MUID:21156231; PMID:11258796
 A; Accession: E90876
 A; Status: preliminary
 A; Residues: 1-124 <HAY>
 A; Cross-references: GB:BA000007; PIDN:BAB35404.1; PID:913361446; GSPDB:GN00154

A;Experimental source: strain 0157:H7, substrain RIMD 0509952
 C;Genetics:
 A;Gene: ECs1981

Query Match 100.0%: Score 21; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 104 HARL 107

RESULT 41

T49512
 hypothetical protein B14D6_640 [imported] - Neurospora crassa

C;Species: Neurospora crassa
 C;Accession: T49512
 C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
 R;Schulte, U.; Align, V.; Hoheisel, J.; Brandt, P.; Furtmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, May 2000
 A;Reference number: Z25022
 A;Accession: T49512
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-125 <SCH2>
 A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6..640
 A;Experimental source: BAC clone B14D6; strain OR74A
 C;Genetics:
 A;Gene: NCSP:B14D6..640
 A;Map position: 6
 C;Superfamily: Neurospora crassa hypothetical protein B14D6..640

Query Match 100.0%: Score 21; DB 2; Length 125;
 Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 11 HARL 14

RESULT 42

PC2265
 cytochrome P450 protein, CYP4H5 - Anopheles albimanus (fragment)

C;Species: Anopheles albimanus
 C;Accession: PC2265
 C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 11-Jun-1999
 R;Scott, J.A.; Collins, F.H.; Feuerstein, R.
 Biochem. Biophys. Res. Commun. 205, 1452-1459, 1994
 A;Title: Diversity of cytochrome P450 genes in the mosquito, Anopheles albimanus.
 A;Reference number: PC2267; MUID:95100981; PMID:7545968
 A;Accession: PC2265
 A;Molecule type: DNA
 A;Residues: 1-127 <SCO>
 A;Cross-references: GB:L38686; NID:g605609; PIDN:AAA65831..1; PID:g605610
 C;Genetics:
 A;Gene: CYP415
 C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
 C;Keywords: heme

RESULT 43

B91218
 thioredoxin 1 [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)

Qy 1 HARL 4
 Db 41 HARL 44

RESULT 44

C86064
 thioredoxin 1 [imported] - Escherichia coli (strain 0157:H7, substrain EDL933)
 C;Species: Escherichia coli
 C;Accession: C86064
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glassner, J.D.; Rose, D.J.; Maller, L.; Grobebeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: C86064
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-127 <STO>
 A;Cross-references: GB:AE005174; NID:91251861; PIDN:AAG58975..1; GSPDB:GN00145; UWGP
 A;Experimental source: strain 0157:H7, substrain EDL933

C;Genetics:
 C;Gene: ttxA
 C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%: Score 21; DB 2; Length 127;
 Best Local Similarity 100.0%; Pred. No. 2e+02; 0; Mismatches 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 9 HARL 12

RESULT 45

G72460
 hypothetical protein APE2331 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix
 C;Accession: G72460
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J
 DNA Res. 5, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix K1
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: G72460
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-129 <RAW>
 A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BA81343..1; PID:d1045129; PID::

A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE331

Query Match 100.0%; Score 21; DB 2; Length 129;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 44 HARL 47

RESULT 46

Q0EC8 hypothetical protein D-132 - Escherichia coli plasmid pBR322

C;Species: Escherichia coli
 C;Accession: 31-Dec-1980 #sequence_revision 31-Dec-1980 #text_change 10-Sep-1999
 R;Sutcliffe, J.G.
 Cold Spring Harb. Symp. Quant. Biol. 43, 77-90, 1979
 A;Title: Complete nucleotide sequence of the Escherichia coli plasmid pBR322.
 A;Reference number: A00923; MUID:80002802; PMID:383387
 A;Accession: A04481
 A;Molecule type: DNA
 A;Residues: 1-132 <sur>
 C;Genetics:
 C;Superfamily: Escherichia coli plasmid pBR322 hypothetical 15.3K protein

Query Match 100.0%; Score 21; DB 1; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 32 HARL 35

RESULT 47

G84669 hypothetical protein At2g27180 [imported] - Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C;Accession: G84669
 C;Species: Mycobacterium leprae
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
 R;Smith, D.R.; Roilson, K.
 submitted to the EMBL Data Library, November 1993
 A;Description: Mycobacterium leprae cosmid B1177.
 A;Reference number: S72720
 A;Accession: S72720
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-133 <EMI>
 A;Cross-references: EMBL:U00011; NID:9466807; PIDN:AAA17084.1; PID:9466809
 C;Genetics:
 A;Start codon: GTG

Query Match 100.0%; Score 21; DB 2; Length 133;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 116 HARL 119

RESULT 50

B83475 hypothetical protein PA133 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: B83475
 R;Stoyer, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;
 adam, S.; Yuan, Y.; Brody, L.B.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.;
 lorry, S.; Olson, M.V.
 Nature 405, 939-944, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A;Reference number: A82950; MUID:20437337; PMID:10984043
 A;Accession: B83475
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-137 <STO>
 A;Cross-references: GB:AE004565; GB:AE004091; NID:99947294; PIDN:AG04742.1; GSPDB:G07498
 C;Genetics:
 A;Experimental source: strain PA01
 C;Gene: PA1353

RESULT 48

T07498 hypothetical protein 133 - Japanese black Pine chloroplast

C;Species: chloroplast Pinus thunbergiana (Japanese black pine)

Wed Nov 13 13:45:32 2002

us-09-697-590-2_copy_292_295.rpr

Page 12

Query Match Similarity 100.0%; Score 21; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
Db 53 HARL 56

Search completed: November 13, 2002, 13:41:39
Job time : 17 secs

us-09-697-590-2_copy_292_295.rsp

Copyright (c) 1993 - 2002 Compugen Ltd.	GenCore version 5.1.3
On protein - protein search, using sw model	
Run on : November 13, 2002, 13:23:38 ; Search time 10 Seconds	(without alignments) 16.591 Million cell updates/sec
Title: US-09-697-590-2_COPY_292_295	
Perfect score: 21	
Sequence: 1 HARL 4	
Scoring table: BLOSUM62	
Searched: Gapop 10.0 , Gapext 0.5	
Total number of hits satisfying chosen parameters: 112892	
Minimum DB seq length: 0	
Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0%	
Maximum Match 100%	
Listing first 45 summaries	
Database : SwissProt_40;*	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
Result No. Score Query Match Length DB ID Description	Summaries
1 21 100.0 71 Y658_ARCFU 029560 archaeoglob	
2 21 100.0 83 E598_HUMAN 029561 homo sapien	
3 21 100.0 93 VP44_BPRAS 029562 mus musculus	
4 21 100.0 107 MBRG_ECOLI 029563 bacteriophila	
5 21 100.0 116 CHPB_ECOLI 029564 escherichia	
6 21 100.0 116 VYLTYCIV 029565	
7 21 100.0 121 YD92_SCOP 029566	
8 21 100.0 122 RL18_MCYCLE 029567	
9 21 100.0 132 YPBL_ECOLI 029568 mycobacterium	
10 21 100.0 133 Y145_ADE07 029569 escherichia	
11 21 100.0 141 NTFD_RHIT 029570 human adeno	
12 21 100.0 155 RS19_DROME 029571 rhizobium l	
13 21 100.0 162 YBIO_ECOLI 029572	
14 21 100.0 163 PTPA_WCTCU 029573	
15 21 100.0 169 RGC2_BP186 029574	
16 21 100.0 182 REGA_AECAC 029575	
17 21 100.0 197 DCTD_CABEL 029576	
18 21 100.0 197 R334_BSP1 029577	
19 21 100.0 207 CORE_XANCP 029578	
20 21 100.0 207 CORE_XYFLA 029579	
21 21 100.0 208 FUSD_BURCE 029580	
22 21 100.0 208 KTH1_AERRE 029581	
23 21 100.0 224 DK44_HUMAN 029582	
24 21 100.0 226 BI02D_XYFLA 029583	
25 21 100.0 236 YF2C_STRAU 029584	
26 21 100.0 241 HUTC_KLEAE 029585	
27 21 100.0 248 Y731_RALSO 029586	
28 21 100.0 256 CB4A_LICES 029587	
29 21 100.0 258 KC2C_VRAS7 029588	
30 21 100.0 261 CB4_SPTOL 029589	
31 21 100.0 266 NFM_KLEBN 029590	
32 21 100.0 268 TP32_TRBPA 029591	
33 100.0 0 07950 treponema p 029592	
RESULT 1	ALIGNMENTS
Y698_ARCFU	
ID Y698_ARCFU	STANDARD;
AC O29560;	PRT; 71 AA.
DT 02/05/60;	
DT 16-OCT-2001 (Rel. 40, last sequence update)	
DT 16-OCT-2001 (Rel. 40, last annotation update)	
DE AFG698.	
GN Archaeoglobus fulgidus.	
OS Archaeae; Burarchaeota; Archaeoglobales;	
OC Archaeoglobaceae; Archaeoglobi; Archaeoglobales;	
OX NCBI TAXID=2334;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=VC-16 / DSM 4304 / ATCC 41558;	
RX MEDLINE=98049343; PubMed=939475;	
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.F., Keckhun K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Karpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Overbeek R., Gocayne J.D., McNeil L.K., Badger J.H., Glodek A., Zhou L., Cottam M.D., Spriggs T., Artlach P., Kaine B.P., Sykes S.M., Sodjo P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Ventter J.C.; "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.", Nature 390:364-370(1997).	
RA RL	
CC 032999 mycobacterium	
CC P03852 escherichia	
CC P05667 human adeno	
CC P00465 rhizobium l	
CC P39018 drosophila	
CC P75816 escherichia	
CC Q10507 mycobacteri	
CC P21678 bacteriophaga	
CC Q08784 acetobacter	
CC P30648 caenorhabdi	
CC P06227 bacteriophaga	
CC Q56764 xanthomonas	
CC Q9pa12 xylella fas	
CC P24129 Burkholderi	
CC Q9ya48 aeropyrum p	
CC Q9ubt3 homo sapien	
CC Q9pal9 xylella fas	
CC P14503 staphylococ	
CC P12380 klebsiella	
CC Q8xva0 ralstonia s	
CC P27524 lycopersico	
CC P38930 saccharomyces	
CC P36494 spinacia ol	
CC P08534 Klebsiella	
CC Q07950 treponema p	
RESULT 2	
ES98_HUMAN	

RESULT 3

EST8_MOUSE STANDARD; PRT; 83 AA.

ID EST8_MOUSE STANDARD; PRT; 83 AA.

AC P58686; [1]

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein EST00098.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TAXID=9606;

[1] SEQUENCE FROM N.A.

RP TISSUE=Muscle;

RA strausberg R.;

RA Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

RN [2] SEQUENCE OF 27-83 FROM N.A.

RX MEDLINE=9929247; PUBMED=10369878;

RA Gilley J., Fried M.;

RT "Extensive gene order differences within regions of conserved synteny between the Fugu and human genomes: Implications for chromosomal evolution and the cloning of disease genes.";

RL Hum. Mol. Genet. 8:1313-1320(1999).

CC -!- SIMILARITY: BELONGS TO THE UPR0184 (EST00098) FAMILY.

CC -!- SIMILARITY: BELONGS TO THE UPR0184 (EST00098) FAMILY.

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CC EMBL; B0001857; AAR01857.1; -.

DR EMBL; BGNC;I7823; C9orf16.

DR InterPro; IPR05374; UPF0184.

DR Pfam; PF03670; UPF0184.1.

KW Hypothetical protein; Coiled coil.

FT DOMAIN 25 74 COILED COIL (POTENTIAL).

FT CONFLICT 35 35 L->V (IN REF. 2).

FT SEQUENCE 83 AA; 9054 MW; EBE1D0AFAAD6DABB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 83; Best Local Similarity 100.0%; Pred. No. 52; Mismatches 0; Indels 0; Gaps 0; Matches 4; Conservative 4; Putative Protein P44.

QY 1 HARL 4

Db 53 HARL 56

RESULT 4

VP44_BPAPS STANDARD; PRT; 93 AA.

ID VP44_BPAPS STANDARD; PRT; 93 AA.

AC Q9T104; [1]

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Putative protein P44.

GN 44.

OS Bacteriophage APSE-1.

OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae; unclassified Podoviridae.

OX NCBI_TAXID=106199;

RN [1]

SEQUENCE FROM N.A.

RX MEDLINE=99420383; PUBMED=10489345;

RA van der Wolk F., Dullemans A.M., Verbeek M., van den Heuvel J.F.J.M.;

RA Isolation and characterization of APSE-1, a bacteriophage infecting

RT the secondary endosymbiont of acyrthosiphon pisum.;

RL virology 262:104-113(1999).

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CC EMBL; AF157835; AAF03987.1; -.

DR

us-09-697-590-2_copy_292_295.rsp

KW Hypothetical protein; SQ 93 AA; 10356 MW; B7EEE57CB8BB3C63 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 93;

Best Local Similarity 100.0%; Pred. No. 59;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HRL 4
Db 67 HRL 70

RESULT 5

MPEC_ECOLI STANDARD; PRT; 107 AA.

ID MPEC_ECOLI P1365; Score 21; DB 1; Length 116;

AC P33647; Score 21; DB 1; Length 116;

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-MAY-1992 (Rel. 22, Last annotation update)

DE Mobilization protein mbec.

GN MPEC.

OS Escherichia coli.

OG Plasmid ColE1.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE=89364735; PubMed=2671664;

RX "Characterization of the ColE1 mobilization region and its protein products";

RT Boyd A.C., Archer J.A.K., Sherratt D.J.;
RL Mol. Gen. Genet. 217:488-498(1989).

CC -!- FUNCTION: THIS PROTEIN IS ESSENTIAL TO PROMOTE THE SPECIFIC TRANSFER OF THE PLASMID IN THE PRESENCE OF CONJUGATIVE PLASMIDS.

CC -!- SIMILARITY: HIGH, TO THE MBEC AND MBKC PROTEINS OF E. COLI.

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CC DR EMBL; X15873; CAA33882.1; -.

CC DR PIR; J00389; J00389.

CC KW Plasmid; Mobility protein; Conjugation.

SQ SEQUENCE 107 AA; 11856 MW; 1372246AD3472182 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 107;

Best Local Similarity 100.0%; Pred. No. 68;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HRL 4
Db 11 HRL 14

RESULT 6

CHPB_ECOLI STANDARD; PRT; 116 AA.

ID CHPB_ECOLI P33647; Score 21; DB 1; Length 116;

AC P33647; Score 21; DB 1; Length 116;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE PeMK-like protein 2.

GN CHPB OR CHBK OR B4225.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OX NCBI_TaxID=562;

RN [1]

RESULT 7

SEQUENCE FROM N.A.

RP STRAIN=K12;

RC MEDLINE=94042047; PubMed=8226627;

RX Masuda Y., Miyakawa K., Nishimura Y., Ohtsubo E.;
RA "chpA and chpB, Escherichia coli chromosomal homologs of the pem locus responsible for stable maintenance of plasmid R100.;"
RT J. Bacteriol. 175:6850-6856(1993).

RL [2]

RN SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=95334362; PubMed=7610040;

RA Bulland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 97.8 through 100 minutes";
RL Nucleic Acids Res. 23:2105-2119(1995).

RN [3]

RP SEQUENCE OF 1-30 FROM N.A.

RC STRAIN=K12;

RX MEDLINE=8627038; PubMed=3525538;

RA Weiss D.I., Johnson D.T., Weith H.L., Somerville R.L.;
RT "Structural analysis of the iler locus of Escherichia coli K12.;"
RL J. Biol. Chem. 261:9966-9971(1986).

RP [4]

RC SEQUENCE OF 20-116 FROM N.A.

RX STRAIN=K12;

RX MEDLINE=8905923; PubMed=2849015;

RA Lahes R., Pirkkaanta T., Valve E., Ilta I., Kukko-Kalske E.,
RA Heilonen J.;
RT "Cloning and characterization of the gene encoding inorganic pyrophosphatase of Escherichia coli K-12.;"
RL J. Bacteriol. 170:5901-5907(1988).

RN [5]

RP GENE MAPPING

RX MEDLINE=94364970; PubMed=8083180;

RA Masuda Y., Onitsuka E.;
RT "Mapping and disruption of the chpB locus in Escherichia coli.;"
RL J. Bacteriol. 176:5861-5863(1994).

CC -!- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF CELL GROWTH. IT ACT AS A GROWTH INHIBITOR. BOTH CHPS AND CHPB BIND TO THE PROMOTER REGION OF THE CHPSB OPERON TO AUTOREGULATE THEIR SYNTHESIS.

CC -!- SIMILARITY: BELONGS TO THE PEAK FAMILY.

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CC DR EMBL; D16451; BAA03920.1; -.

CC DR EMBL; D16451; BAA03920.1; -.

CC DR EMBL; M14018; -; NOT_ANNOTATED_CDS.

DR EMBL; U14003; AAA9122.1; -.

DR EMBL; AR000494; AAC77182.1; -.

DR EMBL; M23550; -; NOT_ANNOTATED_CDS.

DR PIR; D49339; D49339.

DR Ecogene; EG1096; chpb.

DR InterPro; IPR003477; PeMK.

DR Pfam; PF02452; PeMK; 1.

DR DNA-binding; Complete proteome.

SQ SEQUENCE 116 AA; 12492 MW; 4D641F3E302FCF58 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 116;

Best Local Similarity 100.0%; Pred. No. 75;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HRL 4
Db 89 HRL 92

YVL_TYLCV
ID YVL_TYLCV STANDARD; PRT; 116 AA.
AC P27269;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Hypothetical 13.5 kDa protein (VI protein).
GN VI.
OS Tomato yellow leaf curl virus (TYLCV); Begomovirus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TAXID=10832;
RN [1] SEQUENCE FROM N.A.
RX MEDLINE=92024070; PubMed=1926771;
RA Navot N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
RT "Tomato Yellow leaf curl virus: a whitefly-transmitted geminivirus with a single genomic component.";
RL Virology 185:151-161(1991).
CC
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CC
EMBL; X15656; CAA33687.1; --.
DR PIR: E40779; DOCVBL; Geminil_VI.
DR InterPro; IPR02351; Geminil_VI.
DR Pfam; PF01524; Geminil_VI; 1.
DR Pfam; PF03715; WCCH; 1.
DR Prodom; P0002918; Geminil_VI; 1.
KW Hypothetical protein.
SQ SEQUENCE 116 AA; 13459 MW; D506FB53AAF534BB CRC64;
QY 1 HARL 4
DB 65 HARL 68
RESULT 8
ID YDM2_SCHPO STANDARD; PRT; 121 AA.
AC P87133;
DT 15-JUL-1998 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein C57A7.02C in Chromosome 1.
GN SPAC57A7.02C OR SPA167.06C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Schizosaccharomycetes; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TAXID=496;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=TN;
RX MEDLINE=2128732; PubMed=11234002;
RA Cole S.T., Egli M., Garnier T., Churcher C., Harris D.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Connor R.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Durby S., Feltwell T., Fraser A., Hamlin N.,
RA Hollroyd S., Hornsby T., Jigels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skilton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G., Barrell B.G.,
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -I- FUNCTION: THIS IS ONE OF 3 PROTEINS THAT MEDIATE THE ATTACHMENT OF
THE 5S RNA INTO THE LARGE RIBOSOMAL SUBUNIT (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
CC
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CC
EMBL; AL03248; CAA22851.1; --.
DR EMBL; AL03248; CAA22851.1; --.
KW Hypothetical protein.
SQ SEQUENCE 121 AA; 13357 MW; 0461FD5759REB117 CRC64;
QY 1 HARL 4
DB 35 HARL 38
RESULT 9
ID RL8_MYCLE STANDARD; PRT; 122 AA.
AC 032999;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L18.
GN RPLR OR ML1843 OR MLCB2492.20.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TAXID=1769;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=TN;
RX MEDLINE=2128732; PubMed=11234002;
RA Cole S.T., Egli M., Garnier T., Churcher C., Harris D.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Connor R.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Durby S., Feltwell T., Fraser A., Hamlin N.,
RA Hollroyd S., Hornsby T., Jigels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skilton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G., Barrell B.G.,
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -I- FUNCTION: THIS IS ONE OF 3 PROTEINS THAT MEDIATE THE ATTACHMENT OF
THE 5S RNA INTO THE LARGE RIBOSOMAL SUBUNIT (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE L18P FAMILY OF RIBOSOMAL PROTEINS.
CC
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DR EMBL; Z98756; CAB11452.1; -;
 DR EMBL; AL583923; GAC30797.1; ALT_INIT.
 DR Leprona; ML1843; -;
 DR InterPro; IPR001389; L18_bact.
 DR InterPro; IPR001449; Ribosomal_L18p.
 DR Pfam; PF00861; Ribosomal_L18P; 1.
 DR ProDom; PDD01394; Ribosomal_L18P; 1.
 DR TIGRFAMS; TIGR00060; L18_bact; 1.
 DR Ribosomal protein; rRNA-binding; Complete Proteome.
 KW SEQUENCE 122 AA; 13275 MW; FA3C34CA7063AAR CRC54;

SQ

Query Match 100.0%; Score 21; DB 1; Length 122;
 Best Local Similarity 100.0%; Pred. No. 79; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4
 |||||
 Db 17 HARL 20

RESULT 10

YPBL_ECOLI STANDARD; PRT; 132 AA.

ID AC DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Hypothetical 15.3 kDa protein.
 OS Escherichia coli.
 OG Plasmid PB332.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TAXID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80002802; PubMed=383387;

RJ Sutcliffe J.G.;
 RT *Complete nucleotide sequence of the Escherichia coli plasmid
 RL Cold Spring Harb. Symp. Quant. Biol. 43:77-90(1979).

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AC P05667;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE Hypothetical 14.5 kDa early protein.
 CC Human adenovirus type 7.
 CC viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OC RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Gomen;
 RX MEDLINE=83188660; PubMed=6301944;
 RA Engler J.A.; Hoppe M.S.; van Bree M.P.;
 RT "The nucleotide sequence of the genes encoded in early region 2b of
 human adenovirus type 7.";
 RL Gene 21:145-159(1983).

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AC DR EMBL; X03000; CAA26771.1; -;
 KW HYPOTHETICAL PROTEIN; Early protein.
 SQ SEQUENCE 133 AA; 14557 MW; 3085A33IC09060D1 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 86; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4
 |||||
 Db 95 HARL 98

RESULT 12

NIFD_RHILT STANDARD; PRT; 141 AA.

ID NIFD_RHILT
 ID NIFD_RHILT
 AC P00465;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Nitrogenase molybdenum-iron protein alpha chain (EC 1.18.6.1)
 DE (Nitrogenase component I) (dinitrogenase) Fragment.
 GN NIFD.
 OS Rhizobium leguminosarum (biovar trifolioli).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC OC Rhizobiaceae; Rhizobium.
 OX NCBI_TAXID=306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SU329;
 RX MEDLINE=83261209; PubMed=6307623;
 RA Scott K.F.; Rolfe B.G.; Shine J.;
 RT "Biological nitrogen fixation: primary structure of the Rhizobium
 trifolioli iron protein gene.";
 RL DNA 2:149-155(1983).

-1 FUNCTION. THE KEY ENZYMATIC REACTIONS IN NITROGEN FIXATION ARE
 CC CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
 CC IRON PROTEIN AND THE MOYBODIUM-IRON PROTEIN.
 CC -1 CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H⁺ + Ni²⁺ + 16 ATP
 CC = 8 oxidized ferredoxin + 2 NH₃ + 16 ADP + 16 phosphate.
 CC -1 SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS THAT BINDS
 CC 30-32 FE, 2 MO, AND INORGANIC SULFUR.
 CC -1 SIMILARITY: BELONGS TO THE NIFD/NIFR/NIFE/NIFN FAMILY.

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CC
CC
CC
DR
DR
PIR: A00543; NIZRAT.

DR HSSP; P07328; 3MIN.

DR InterPro; IPR000318; Nitrogenase_compl.

DR Pfam; PF00148; oxidored_nitro; 1.

DR PROSITE; PS00090; NITROGENASE_1-2; PARTIAL.

DR PROSITE; PS00599; NITROGENASE_1-1; 1.

KW Oxdoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur.

FT NON_TER; 141 141

SQ SEQUENCE 141 AA; 15524 MW; A89CE780C577A40E CRC64;

Query Match 100.0%; Score 21; DB 1; Length 141;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 HARL 15

RESULT 13

RS19_DROME RS19_DRDOME STANDARD; PRT; 155 AA.

AC P39018; DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DE 40S ribosomal protein S19.

GN RPS19.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryote; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

OC Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.

NCBI_TaxID:7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Centon-S;

RX MEDLINE=33376521; PubMed=8367309;

RA Baumgartner S.W., Martin D., Chiquet-Ehrismann R.;

RT "Drosophila ribosomal protein S19 cDNA sequence.";

RL Nucleic Acids Res. 21:3887-3887(1993).

CC -----
-1- SIMILARITY: BELONGS TO THE S19E FAMILY OF RIBOSOMAL PROTEINS.

CC -----
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CC -----
EMBL; X73153; CAA1677; J;

DR Flybase; FBgn0010412; Rpp19.

DR InterPro; IPR001266; Ribosomal_S19E.

DR Pfam; PF01090; Ribosomal_S19_E; 1.

DR ProDom; PDD003954; Ribosomal_S19_E; 1.

DR PROSITE; PS00528; RIBOSOMAL_S19E; 1.

KW Ribosomal protein.

FT INIT_MET 0 BY SIMILARITY.

SQ SEQUENCE 155 AA; 17174 MW; F77AB02833E779F CRC64;

Query Match 100.0%; Score 21; DB 1; Length 155;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HARL 4

Db 108 HARL 111

RESULT 14

YBJO_ECOLI

ID YBJO_ECOLI

STANDARD;

PRT; 162 AA.

AC P75815;

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein YBJO.

GN YBJO OR B0558 OR Z1005 OR ECS0938.

OS Escherichia coli, and

OC Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562, 83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=91426617; PubMed=9278503;

RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,

Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

Riley M., Colwell L., Goeden M.A., Rose D.J.,

Mau B., Shao Y.,

RA "The complete genome sequence of Escherichia coli K-12.";

RN Science 277:1453-1474(1997).

RP [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=91051202; PubMed=8905232;

RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,

RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,

RA Kimura S., Kitagawa M., Makino K., Masuda S., Mikai T., Mizobuchi K.,

RA Mori I., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,

RA Samegi T., Sekii Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,

RA Yano M., Horie T., "A 7.18-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";

RL DNA Res. 3:137-155(1996).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / ED1933 / ATCC 700927;

RX MEDLINE=21074935; PubMed=11206551;

RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirpatrick H.,

RA Posfai G., Hackert J., Klink S., Bourlin A., Shao Y., Miller L.,

RA Grotnbeck J.E., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

RA Welch R.A., Blattner F.R.,

RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";

RL Nature 409:529-533(2001).

[4] RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / RIMD 0509952;

RX MEDLINE=21156231; PubMed=1125896;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Iida T., Takami H., Honda T., Sakakawa C., Ogasawara N., Yasunaga T.,

RA Kuwara S., Shiba T., Hattori M., Shinagawa H.,

RA "Complete genome sequence of enterohaemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";

RA DNA Res. 8:11-22(2001).

CC -----
-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

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CC EMBL; AE000187; AAC73945.1; -.

QY 1 HARL 4 DT 01-APR-1993 (Rel. 25, Last sequence update)
 ||||| DE 15-JUN-2002 (Rel. 41, Last annotation update)
 ID RECA_ACAC STANDARD; PRT; 182 AA.
 AC 008784; DE probable deoxycytidylate deaminase (EC 3.5.4.12) (dCMP deaminase).
 Db 143 HARL 146 GN ZK643.2.
 RESULT 17 OS Caenorhabditis elegans.
 RECA_ACAC STANDARD; PRT; 182 AA.
 ID RECA_ACAC STANDARD; PRT; 182 AA.
 AC 008784; DE probable deoxycytidylate deaminase (EC 3.5.4.12) (dCMP deaminase).
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 16-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RecA protein (Recombinase A) (Fragment).
 GN
 OS Acetobacter aceti.
 OC Bacteria: Proteobacteria; alpha subdivision; Acetobacteraceae;
 OC Acetobacter.
 OX NCBI_TAXID=435;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=BRISTOL N2;
 RX MEDLINE=92168156; PubMed=153879;
 RA Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,
 RA Halloran N., Green P., Thierry-Mieg J., Oiu L., Dear S., Coulson A.,
 RA Craxton M., Durbin R., Berks M., Metzstein M., Hawkins T.,
 RA Ainscough R., Waterston R.;
 RT Nature 356:37-41 (1992).
 RL "The C. elegans genome sequencing project: a beginning."
 CC FUNCTION: SUPPLIES THE NUCLEOTIDE SUBSTRATE FOR THYMIDYLATE
 CC SYNTHETASE (BY SIMILARITY).
 CC CATALYTIC ACTIVITY: dGMP + H(2)O = dUMP + NH(3).
 CC COFACTOR: ZINC (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CYTIDINE AND DEOXYCYTIDYLATE DEAMINASES
 CC FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; S23240;
 DR PIR; S23240;
 DR WORMPEP; 20643.2; CE00441;
 DR InterPro; IPR003125; DCMP/cyt_deam.
 DR Pfam; PF00383; DCMP_cyt_deam; 1.
 DR PROSITE; PS00903; CYT_DCMP_DEAMINASES; 1.
 DR KW HYPOTHETICAL PROTEIN; Hydrolase; Nucleotide biosynthesis; Zinc.
 FT METAL 117 117 ZINC (BY SIMILARITY).
 FT METAL 143 143 ZINC (BY SIMILARITY).
 FT METAL 146 146 ZINC (BY SIMILARITY).
 SQ SEQUENCE 197 AA; 22528 MW; 33B6A723AD3FF9E7 CRC64;
 Query Match 10.0%; Score 21; DB 1; Length 197;
 Best Local Similarity 10.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 FT NON_TER 1 1
 FT SEQUENCE 182 AA; 19687 MW; 3251807B73877E90 CRC64;
 SQ
 Query Match 100.0%; Score 21; DB 1; Length 182;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 DB 57 HARL 60
 RESULT 19
 RECA_BPSPI STANDARD; PRT; 197 AA.
 ID RECA_BPSPI STANDARD; PRT; 197 AA.
 AC 006227;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE RNA polymerase sigma GP34 factor.
 GN 34
 OS Bacteriophage SP01.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC SP01-like viruses.
 OX NCBI_TAXID=10685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85134870; PubMed=6441846;
 RA Costanzo M., Brzustowicz L., Haennett N., Pero J.; primary structure
 RT of genes encoding regulatory subunits of *Bacillus subtilis* RNA
 of genes encoding regulatory subunits of *Bacillus subtilis* RNA

RESULT 24		Db	212 HARL 215
ID	DKK4_HUMAN	STANDARD:	PRT; 224 AA.
AC	Q9UBP3; Q9Y4C3;	PRT;	224 AA.
DT	16-OCT-2001 (Rel. 40, Created)	STANDARD:	PRT; 226 AA.
DT	16-OCT-2001 (Rel. 40, Last sequence update)	STANDARD:	PRT; 226 AA.
DT	15-JUN-2002 (Rel. 41, Last annotation update)	STANDARD:	PRT; 226 AA.
DE	Dickkopf related protein-4 precursor (Dkk-4)	STANDARD:	PRT; 226 AA.
GN	DKK4	STANDARD:	PRT; 226 AA.
OS	Homo sapiens (human)	STANDARD:	PRT; 226 AA.
OC	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Xenelia fastidiosa.	STANDARD:	PRT; 226 AA.
OX	NCBI_TaxID=9606;	STANDARD:	PRT; 226 AA.
RN	[1] SEQUENCE FROM N.A., AND SEQUENCE OF 19-28 AND 134-144.	STANDARD:	PRT; 226 AA.
RP	SEQUENCE FROM N.A.	STANDARD:	PRT; 226 AA.
RX	MEDLINE-20035735; Pubmed-10570958;	STANDARD:	PRT; 226 AA.
RX	MEDLINE-20035735; Pubmed-10570958;	STANDARD:	PRT; 226 AA.
RX	Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickerling T.W., Duong T., Goodearl A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.; Amaravadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B., Family;" Functional and structural diversity of the human Dickkopf gene [2]. Gene 238:301-313(1999).	STANDARD:	PRT; 226 AA.
RP	SEQUENCE FROM N.A.	STANDARD:	PRT; 226 AA.
RA	Tate G., Mitsuya T.; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.	STANDARD:	PRT; 226 AA.
RA	"Human Dickkopf as well as DAN family members, Cerberus and Gremlin, are preferentially expressed in the epithelial malignant cell lines.";	STANDARD:	PRT; 226 AA.
RA	J. Biochem. Mol. Biol. Biophys. 3:239-242(1999).	STANDARD:	PRT; 226 AA.
RA	[3] SEQUENCE FROM N.A.	STANDARD:	PRT; 226 AA.
RA	Tate G., Suuki T., Mitsuya T.; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.	STANDARD:	PRT; 226 AA.
RA	"Human Dickkopf as well as DAN family members, Cerberus and Gremlin, are preferentially expressed in the epithelial malignant cell lines.";	STANDARD:	PRT; 226 AA.
RA	J. Biochem. Mol. Biol. Biophys. 3:239-242(1999).	STANDARD:	PRT; 226 AA.
RA	-!- FUNCTION: INHIBITOR OF WNT SIGNALING PATHWAY.	STANDARD:	PRT; 226 AA.
CC	-!- SUBCELLULAR LOCATION: Secreted.	STANDARD:	PRT; 226 AA.
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN CEREBELLUM, T-CELLS, ESOPHAGUS, AND LUNG.	STANDARD:	PRT; 226 AA.
CC	-!- PFM: APPEARS NOT TO BE GLYCOSYLATED.	STANDARD:	PRT; 226 AA.
CC	-!- PFM: CAN ALSO BE PROTEOLYTICALLY PROCESSED BY A FURIN-LIKE PROTEASE.	STANDARD:	PRT; 226 AA.
CC	-!- SIMILARITY: BELONGS TO THE DICKKOPF FAMILY.	STANDARD:	PRT; 226 AA.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).	STANDARD:	PRT; 226 AA.
CC	-!- CATALYTIC ACTIVITY: ATP + 7,8-diaminononanoate + CO(2) = ADP + Phosphate + dethiobiotin.	STANDARD:	PRT; 226 AA.
DR	EMBL: AF177397; BAA2677_1; -.	STANDARD:	PRT; 226 AA.
DR	EMBL: AB018005; BAA3475_1; -.	STANDARD:	PRT; 226 AA.
DR	EMBL: AB018003; BAA3475_1; JOINED.	STANDARD:	PRT; 226 AA.
DR	EMBL: AB018004; BAA3475_1; JOINED.	STANDARD:	PRT; 226 AA.
DR	EMBL: AB017788; BAA3438_1; -.	STANDARD:	PRT; 226 AA.
DR	EMBL: P25687; 1IMT; Genevar: HGNC:2804; DKK4.	STANDARD:	PRT; 226 AA.
DR	MIM: 605417; -.	STANDARD:	PRT; 226 AA.
FT	Developmental protein; Signal.	STANDARD:	PRT; 226 AA.
FT	SIGNAL 1 18	STANDARD:	PRT; 226 AA.
FT	CHAIN 19 224 DICKKOPF RELATED PROTEIN-4. SHORT FORM.	STANDARD:	PRT; 226 AA.
FT	DOMAIN 1 90 DICK-K-TYPE CYS-1.	STANDARD:	PRT; 226 AA.
FT	DOMAIN 145 218 DRK-TYPE CYS-2.	STANDARD:	PRT; 226 AA.
FT	CONFLICT 93 M > L (IN REF. 3).	STANDARD:	PRT; 226 AA.
FT	SEQUENCE 224 AA; 2487 MW; 45FBBBC4/6961/357 CRC64;	STANDARD:	PRT; 226 AA.
Query Match	100 %; Score 21; DB 1; Length 224;	STANDARD:	PRT; 226 AA.
Best Local Similarity	100.0%; Pred. No. 1.5e+02;	STANDARD:	PRT; 226 AA.
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	STANDARD:	PRT; 226 AA.
QY	1 HARL 4	STANDARD:	PRT; 226 AA.

CC -!- SIMILARITY: BELONGS TO THE UPF0135 (NIF3) FAMILY.

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CC

DR EMBL: AL046072; CAD16638; 1;

FT InterPro: IPR002578; DUF234;

DR Pfam: PF01784; DUF34; 1.

DR TIGRFAMS: TIGR0486; DUF34; 1.

KW HYPOTHETICAL PROTEIN; COMPLETE PROTEOME.

SQ SEQUENCE: 248 AA; 26651 MW; 101E0B25RC353F67 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 248;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HARL 4

Db 80 HARL 83

RESULT 29

CB4A_LYCES STANDARD; PRT; 256 AA.

ID CB4A_LYCES STANDARD; PRT; 256 AA.

AC P27524; (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Chlorophyll A-B binding protein CP24 10A; chloroplast precursor (CAB-DE 10A) (LHCp).

GN CAP0A.

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9135549; PubMed=2103430;

RA Schwartz E.; Pichersky E.

RT *Sequence of two tomato nuclear genes encoding chlorophyll a/b-binding proteins of CP24, a PSII antenna component.*;

RL Plant Mol. Biol. 15:157-160(1990).

CC -!- SIMILARITY: BELONGS TO THE ELIP/PSBS FAMILY.

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EMBL: M22605; AAA4143.1; -

DR PIR: S1877; S1877; Chlоро_ABbind.

DR InterPro: IPR001344; Chlоро_ABbind.

DR Pfam: PF00504; chlоро_ABbind; 1.

DR ProDom: PD00275; Chlоро_ABbind; 1.

KW Chlorophyll; Photosynthesis; Chlоро_ABbind; 1.

FT Chloroplast; transit peptide; Multigene family; Transmembrane.

FT CHAIN ?

FT CLOROPHYL (POTENTIAL). CHLOROPHYL A-B BINDING PROTEIN CP24 10A.

FT SEQUENCE 256 AA; 27253 MW; BD397BE9E48300A CRC64;

Query Match 100.0%; Score 21; DB 1; Length 256;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HARL 4

Db 229 HARL 232

RESULT 30

KC2C_YEAST STANDARD; PRT; 258 AA.

ID KC2C_YEAST STANDARD; PRT; 258 AA.

AC P38930; (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Casein kinase II beta, chain (CK II).

RN GN CKB2 OR YOR039W OR SP26.32.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Saccharomyces cerevisiae; Saccharomyces cerevisiae; Saccharomyces cerevisiae casein kinase II. ";

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94209539; PubMed=8027080;

RA Reed J.C.; Bidwell A.P.; Glover C.V.C.

RT "Cloning and disruption of CKB2, the gene encoding the 32-kDa regulatory beta-subunit of *Saccharomyces cerevisiae* casein kinase II."

RN [2]

RP SEQUENCE FROM N.A.

RX J. Biol. Chem. 269:18192-18200(1994).

RN [3]

RP de Haan M.; Maarse A.C.; Grivell L.A.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE OF 172-258 FROM N.A.

RX STRAIN-AP3;

RA Haider M.; Bitto A.; Wallner J.; Breitenbach M.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

RN [5]

RP PARTIAL SEQUENCE.

RX MEDLINE=94182950; PubMed=8135547;

RA Bidwell A.P.; Reed J.C.; Glover C.V.C.

RT "Casein kinase II of *Saccharomyces cerevisiae* contains two distinct regulatory subunits, beta and beta'";

RL Arch. Biochem. Biophys. 309:348-355(1994).

CC -!- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).

CC -!- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', ONE BETA CHAIN AND ONE BETA' CHAIN.

CC -!- PTM: PHOSPHORYLATED BY ALPHA CHAIN (BY SIMILARITY).

CC -!- PTM: THE N-TERMINUS IS BLOCKED.

CC -!- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.

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EMBL: U08849; AAA21056.1; -

DR EMBL: X87331; CAA60758.1; -

DR EMBL: X82893; CAA58064.1; -

DR SGD; S0005565; CKB2.

DR InterPro: IPR000704; CAS_kinase_II.

DR Pfam: PF01214; CK-II_beta; 1.

DR PRINTS; PR00472; CASEINKINASEII.

DR PROSITE; PS01101; CK_BETA; 1.

KW Transferase; Serine/threonine-protein kinase; Phosphorylation.

SQ SEQUENCE 258 AA; 29842 MW; D606CB3D70B19A4 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 258;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HARL 4
 |||||
 Db 96 HARL 99

RESULT 31
 CB4_SP1OL CB4_SP1OL STANDARD; PRT; 261 AA.
 ID CB4_SP1OL
 AC P36494;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Chlorophyll A-B binding protein CP24, chloroplast precursor.
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN="cv. Monatol"; TISSUE="leaf";
 RA Wedel N.; Klein R.; Herrmann R.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DDBJ databases.
 CC -I SIMILARITY: BELONGS TO THE ELIP/PSSS FAMILY.
 CC
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 CC
 DR InterPro: IPR001344; Chlоро_ABBind.
 DR Pfam: PF00504; chloro_a-b-bind; 1.
 DR Prodom: PD000275; Chlоро_ABind; 1.
 CC Chlorophyll; Photosynthesis; Chlorophyll; Chloroplast; Transit peptide; Transmembrane.
 FT TRANSIT 1 51 CHLOROPLAST (POTENTIAL).
 FT CHAIN 52 261 CHLOROPHYLL A-B BINDING PROTEIN CP24.
 SQ SEQUENCE 261 AA; 27840 MW; A1599f7B626CA1A5 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 261;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 32
 NIFM_KLEPN NIFM_KLEPN STANDARD; PRM; 266 AA.
 ID NIFM_KLEPN
 AC P08534;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE protein nifM.
 GN NIFM.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=8904839; PubMed=3062178;
 RA Arnold W.; Rump A.; Klipp W.; Priester U.B.; Puehler A.;
 RT "Nucleotide sequence of a 24,206-base-pair DNA fragment carrying the
 entire nitrogen fixation gene cluster of Klebsiella pneumoniae.";
 RT J. Mol. Biol. 203:715-738(1988);
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN="cv. Monatol";
 RX MEDLINE=8002825; PubMed=2826155;
 RA Paul W.; Merrick M.J.;
 RA Collet T.A.; White T.; Howard K.; Orme-Johnson W.H.;
 RL Submittted (JUL-1989) to the EMBL/GenBank/DDBJ databases.
 CC SEQUENCE FROM N.A.
 RC STRAIN="cv. Monatol";
 RA Collet T.A.; White T.; Howard K.; Orme-Johnson W.H.;
 RL Submittted (JUL-1989) to the EMBL/GenBank/DDBJ databases.
 CC -I FUNCTION: REQUIRED FOR THE ACTIVATION AND STABILIZATION OF THE
 CC IRON-COMPONENT (NIFH) OF NITROGENASE. PROBABLE PRIME.
 CC -I SIMILARITY: BELONGS TO THE PPIC/PARVULIN FAMILY OF ROTAMASES.
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 CC
 DR EMBL; X05887; CAM29313.1; -.
 DR EMBL; X13303; CAA31679.1; -.
 DR EMBL; M24106; AAA25105.1; -.
 DR PIR; S02510; S02510.
 DR InterPro: IPR00297; Rotamase.
 DR Pfam: PF00659; Rotamase; 1.
 DR PROSITE; PS01096; PPIC_PPASE_1; 1..
 DR PROSITE; PS01918; PPIC_PPASE_2; 1..
 KW Nitrogen Fixation; Isomerase; Rotamase.
 FT DOMAIN 124 221 PPIC.
 SQ SEQUENCE 266 AA; 30012 MW; C151684ED161AABB CRC64;

Query Match 100.0%; Score 21; DB 1; Length 266;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 33
 TP32_TRPA TP32_TRPA STANDARD; PRM; 268 AA.
 ID TP32_TRPA
 AC 007950;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Membrane lipoprotein Tpn32 precursor (29 kDa protein).
 GN TPN32 OR TP021.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 RN
 RP SEQUENCE FROM N.A.
 RA Porcella S.F.; Radolf J.D.; Norgard M.V.;
 RT "Treponema pallidum 29k protein is homologous to a lipoprotein
 present in *Pasteurella hemolytica* and in *Haemophilus influenzae*
 type b.";
 RT Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN-Nichols;
 RA Stann L.V., Barnes N.Y.;
 RT "Treponema pallidum lipoprotein homologue.";
 RL Submitted (JUN-197) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Nichols;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Doolan R., Gwin M., Hickie R., Clayton R., Ketchum K.A.,
 RA Sodergren E., Harham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 spirochete.";
 RL Science 281:375-388(1998).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 (Probable).
 CC -----
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 CC -----
 DR U07358: AAB33362.1; -.
 DR EMBL; U07358; AAB33362.1; -.
 DR EMBL; U03844; AAB01267.1; -.
 DR TIGR; T0821; -.
 DR InterPro; IPR004872; Lipoprotein_9.
 DR Pfam; PF03180; Lipoprotein_9.1.
 DR PROSITE; PS00013; PROKR_LIPOPROTEIN; 1.
 DR Membrane; Lipoprotein; Signal; Complete proteome.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 268 MEMBRANE LIPOPROTEIN TPN32.
 FT LIPID 24 24 N-ACYL GLYCERIDE (POTENTIAL).
 SO SEQUENCE 268 AA; 29081 MW; A02LF8A07A8B691 CRC64;

Query Match 100.0%; Score 21; DB 1; Length 269;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 41 HARL 44

RESULT 35
 ICA4_HUMAN STANDARD; PRT; 271 AA.
 ID ICA4_HUMAN STANDARD; PRT; 271 AA.
 AC 014773; 014771; 014772; 016375;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Intercellular adhesion molecule-4 precursor (ICAM-4) (Landsteiner-Wiener blood group glycoprotein) (LW blood group protein) (CD242 antigen).
 DE ICAM4 OR LW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=94261574; PubMed=8202405;
 RA Bailly P., Hermann P., Callebaut I., Sonneborn H.H., Khamlich S.,
 RA Moron J.-P., Cartron J.-P.;
 RT "The LW blood group glycoprotein is homologous to intercellular adhesion molecules";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:5506-5510(1994).
 RL
 RN [2]
 SEQUENCE FROM N.A.
 RX MEDLINE=9621993; PubMed=8639917;
 RA Hermann P., le Pennec P.Y., Rouger P., Cartron J.-P., Bailly P.;
 RT "Characterization of the gene encoding the human LW blood group protein in LW⁺ and LW⁻ phenotypes.";
 RL Blood 87:2962-2967(1996).
 RN [3]
 SEQUENCE OF 1-130 FROM N.A. AND VARIANT BLOOD GROUP LW(B).
 RX MEDLINE=95359422; PubMed=7632468;
 RA Hermann P., Gane P., Mattei M.-G., Sistonen P., Cartron J.-P.,
 RA Bailly P.;
 DE "Molecular basis and expression of the LWa/LWb blood group polymorphism";
 DE RT Blood 86:1590-1594(1995).
 RP SEQUENCE FROM N.A.
 OC Bacteria; Actinobacteria; Streptomycetaceae; Streptomyces.
 OX NCBI_TAXID=68197;
 RN [1]
 SEQUENCE FROM N.A.
 RA van Cott E.M., Moran L.S., Slatko B.E., Wilson G.G.;
 RT "Characterization of the SfiI restriction and modification genes.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Recognizes the double-stranded sequence GGCCNNNNNGCC
 CC and cleaves before N-9.
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give

CC specific double-stranded fragments with terminal 5'-phosphates.
 CC -----
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 CC -----
 DR EMBL; AF039750; AAB05365.1; -.
 DR REBASE; 1655; SfII.
 DR Hydrolase; Endonuclease; Nuclease; Restriction system.
 CC KW Sequence 269 AA; 31044 MW; 3C4049BAA5205EA CRC64;
 SQ SEQUENCE

CC GROUP ANTIGENS IS A SINGLE VARIATION IN POSITION 100; GLN-100
 CC CORRESPONDS TO LW(A) AND ARG-100 TO LW(B).
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. ICAM
 CC SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC
 CC DR EMBL; L27671; AAA59538.1; -.
 CC DR EMBL; L27670; AAA59537.1; -.
 CC DR EMBL; X93093; CAA3661.1; -.
 CC DR EMBL; S78852; AAB35046.1; -.
 CC DR HSSP; P05362; IICL1.
 CC DR HSSP; P05362; IICL4.
 CC DR IMIM; HGNc; 5347; ICAM4.
 CC DR KW Immunoglobulin domain; Cell adhesion; Glycoprotein; Transmembrane;
 KW Repeat; Signal; Alternative splicing; Polymorphism;
 KW Blood group antigen.
 FT SIGNAL 1 PENTAPOLYMER.
 FT CHAIN 23 INTERCELLULAR ADHESION MOLECULE-4.
 FT DOMAIN 23 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 241 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 262 CYTOPLASMIC (POTENTIAL);
 FT DOMAIN 62 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 146 IG-LIKE C2-TYPE DOMAIN 2.
 FT DISULFID 69 BY SIMILARITY.
 FT DISULFID 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 AWSPPPTIALASGSSLVGLLITVGAYVCKCLAMKSOA.
 FT VARSPLIC 233 O -> GEAPL (IN SHORT ISOFORM).
 FT VARIANT 100 O -> R (IN LW(B)).
 FT CONFLICT 14 29 /PFDWVAR_003912.
 FT SEQUENCE 271 AA; ARAPGPVSEALGRRTK -> RPPTRRELGARWDAGL (IN
 SQ 100.0%; Score 21; DB 1; Length 271;
 Query Match 100.0%; Score 21; DB 1; Length 273;
 Best Local Similarity 100.0%; Prod. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 Db 113 HARL 116
 RESULT 37
 RECA_NEICCI RECA_NEICCI STANDARD; PRT; 274 AA.
 ID 09595; DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Reca protein (Recombinase A) (Fragment).
 GN RECA.
 OS Neisseria cinerea.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 RN NCBI_TaxID=483;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN=LNP 1646;
 RX MEDLINE=97149032; PubMed=8995060;
 RA Feil E., Zhou J., Maynard Smith J., Spratt B.G.;
 RT "A comparison of the nucleotide sequences of the adk and reca genes
 RT of pathogenic and commensal *Neisseria* species: evidence for extensive
 RT interspecies recombination within adk.";
 CC J. Mol. Evol. 43:631-640(1998).
 CC -!- FUNCTION: CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF
 CC SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED
 CC DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYDRIDIZATION OF
 CC HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEVA CAUSING
 CC ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
 CC NUO-32.
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY (BY similarity).
 CC
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 CC
 CC RT "Primary structure of the nuclear-encoded 29.9 kDa subunit of NADH:
 CC ubiquinone reductase from *Neurospora crassa* mitochondria.";
 CC RL Biophys. Acta 1089:389-390(1991).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane; matrix side.
 CC -!- SIMILARITY: BELONGS TO THE COMPLEX I 29.9 kDa SUBUNIT FAMILY.
 CC
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 CC
 CC DR EMBL; X56237; CAA39694.1; -.
 CC DR PIR; S17191; S17191.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide.
 FT TRANSMIT 9 MITOCHONDRIUM.
 FT CHAIN 9 NADH-UBIQUINONE OXIDOREDUCTASE 29.9 KDA
 FT SUBUNIT.
 FT SQ SEQUENCE 273 AA; 30862 MW; 4B117593B47EEFL CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 273;
 Best Local Similarity 100.0%; Prod. No. 1.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 Db 113 HARL 116
 RESULT 37
 RECA_NEICCI RECA_NEICCI STANDARD; PRT; 274 AA.
 ID 09595; DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Reca protein (Recombinase A) (Fragment).
 GN RECA.
 OS Neisseria cinerea.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 RN NCBI_TaxID=483;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN=LNP 1646;
 RX MEDLINE=97149032; PubMed=8995060;
 RA Feil E., Zhou J., Maynard Smith J., Spratt B.G.;
 RT "A comparison of the nucleotide sequences of the adk and reca genes
 RT of pathogenic and commensal *Neisseria* species: evidence for extensive
 RT interspecies recombination within adk.";
 CC J. Mol. Evol. 43:631-640(1998).
 CC -!- FUNCTION: CAN CATALYZE THE HYDROLYSIS OF ATP IN THE PRESENCE OF
 CC SINGLE-STRANDED DNA, THE ATP-DEPENDENT UPTAKE OF SINGLE-STRANDED
 CC DNA BY DUPLEX DNA, AND THE ATP-DEPENDENT HYDRIDIZATION OF
 CC HOMOLOGOUS SINGLE-STRANDED DNAs. IT INTERACTS WITH LEVA CAUSING
 CC ITS ACTIVATION AND LEADING TO ITS AUTOCATALYTIC CLEAVAGE.
 CC NUO-32.
 CC -!- SIMILARITY: BELONGS TO THE RECA FAMILY (BY similarity).
 CC
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 CC

CC
DR EMBL; U57906; RAB49191.1; -.
DR HSSP; P03017; 2REB.
DR InterPro; IPR001553; RecA.
DR Pfam; PF00154; recA; 1.
DR ProDom; PD000229; RecA; 1.
DR PROSITE; PS00321; RECAl_1; 1.
DR PROSITE; PS50162; RECAl_2; 1.
DR PROSITE; PS50163; RECAl_3; 1.
KW DNA damage; DNA recombination; SOS response; ATP-binding; DNA-binding.
FT NON_TER 1 1
NP_BIND 43 50 ATP (BY SIMILARITY).
FT NON_TER 274 AA; 274 274 ATP (BY SIMILARITY).
SEQUENCE SQ 274 AA; 29602 MW; 4E9FC11097339D94 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HARL 4
Db 144 HARL 147

RESULT 38
YG3_SYN3 STANDARD; PRT; 274 AA.
ID YG3_SYN3 STANDARD; PRT; 274 AA.
AC P74261;
DT 15-DEC-1998 (Rel. 37, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE HYPOTHETICAL tRNA/tRNA methyltransferase srl1673 (EC 2.1.1.-).
GN SIRI673
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1] SEQUENCE FROM N.A., AND SEQUENCE OF 1-30; 27-65 AND 229-247.
RN MEDLINE=92405925; PubMed=9260969;
RA Kim S.I., Leem S.-H., Choi J.-S., Chung Y.H., Kim S., Park Y.-M.,
RA Park Y.K., Lee Y.N., Ha K.-S.;
RT "Cloning and characterization of two cata genes in *Actinobacter lwoffii* K24";
RL J. Bacteriol. 179:5226-5231(1997).
CC [-] FUNCTION: CAN CLEAVE 4-METHYL-, 4-CHLORO-, AND 3-METHOXYCATECHOL
CC AT LOWER RATES THAN CATECHOL, BUT HAS NO ACTIVITY WITH 4-NITROCATECHOL OR ROTOCATECHIC ACID.
CC [-] CATALYTIC ACTIVITY: Catechol + O(2) = cis,cis-muconate.
CC [-] COFACTOR: FERRIC ION.
CC [-] PATHWAY: FIRST STEP IN THE DEGRADATION OF CATECHOL TO SUCCINATE
CC AND ACETYL-COA IN THE BETA-KETOAPATE PATHWAY.
CC [-] SUBUNIT: HOMODIMER (POSSIBLY).
CC [-] INDUCTION: BY ANILINE.
CC [-] SIMILARITY: BELONGS TO THE INTRADIOL RING-CLEAVAGE DIOXYGENASE FAMILY.
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CC [-] SIMILARITY: BELONGS TO THE RNA METHYLTRANSFERASE TRMH FAMILY.
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DR EMBL; U77659; AAC31767.1; -.
DR HSSP; P00437; 3PCC.
DR InterPro; IPR000627; Dioxygenase.
DR Pfam; PF00775; Dioxygenase; 1.
DR PROSITE; PS00033; INTRABIOTOL_DIOXYGENAS; 1.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; Dioxygenase; Iron.
FT METAL 158 158 IRON (BY SIMILARITY).
FT METAL 192 192 IRON (BY SIMILARITY).
FT METAL 216 216 IRON (BY SIMILARITY).
FT METAL 218 218 IRON (BY SIMILARITY).
SQ SEQUENCE 275 AA; 30399 MW; 3FB80C12/F45AB07 CRC64;
Query Match 100.0%; Score 21; DB 1; Length 275;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HARL 4
Db 115 HARL 118

RESULT 40
DAFP_PSEAE STANDARD; PRT; 276 AA.
ID DAFP_PSEAE STANDARD; PRT; 276 AA.
AC Q51664;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Diaminopimelate epimerase (EC 5.1.1.7) (DAP epimerase).
DAFP OR PA5278.

Query Match 100.0%; Score 21; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HARL 4
Db 118 HARL 121

us-09-697-590-2_copy_292_295.rsp

OC Pseudomonas aeruginosa
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC NCBI_TaxID=287;
 RN SEQUENCE FROM N.A.
 RN [1]
 RN STRAIN=ATCC 15692 / PAO1;
 RX MEDLINE=2047337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Gohtry L., Tolentino E., Westrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an
 RT opportunistic pathogen.
 RL Nature 406:559-564(2000).
 RN [2]
 RP SEQUENCE OF 169-276 FROM N.A.
 RC STRAIN=7NSK2;
 RX MEDLINE=95231283; PubMed=7715441;
 RA Hoffe M., Dong Q., Kourambas S., Krishnapillai V., Mergeay M.;
 RT "The sss gene product, which affects pvoevdin production in
 Pseudomonas aeruginosa 7NSK2, is a site-specific recombinase."
 RL *Mol. Microbiol.* 14:1011-1020(1994).
 CC -1 - CATALYTIC ACTIVITY: L-L-2,5-diaminohexapeptidate = meso-
 CC -1 - SIMILARITY: BELONGS TO THE DIAMINOPIMELATE EPIMERASE FAMILY.
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 CC -----
 CC EMBL; AE004940; AAG08663.1; - .
 DR EMBL; X18478; CAAS5224.1; - .
 DR HSSP; P44859; 1BWZ.
 DR InterPro; IPR01653; DAP_epimerase.
 DR Pfam; PF01678; DAP_epimerase; 2.
 DR PROSITE; PS01326; DAP_EPIMERASE; 1.
 KW Isomerase; Lysine biosynthesis; Complete proteome.
 FT ACT_SITE 75 75 BY SIMILARITY.
 FT ACT_SITE 219 219 BY SIMILARITY.
 SQ SEQUENCE 276 AA; 32396 MW; 75789FEFF4C3C88E CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 280;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HARL 4
 Db 128 HARL 131
 RESULT 42
 GSTG_BPT5
 ID GSTG_BPT6 STANDARD; PRT; 280 AA.
 AC 006718;
 DT 01-JUN-1994 (Rel. 29, created)
 DT 01-JUN-1994 (Rel. 29, last sequence update)
 DT 01-OCT-1994 (Rel. 30, last annotation update)
 DE Beta-D-glucosyl-HMC-alpha-D-glucosyl-transferase (EC 2.4.1.-).
 DE Bacteriophage T6.
 OS Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC T4-like viruses.
 KW NCBI_TaxID=10666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93219141; PubMed=8464751;
 RA Winkler M., Rueger W.;
 RT "Cloning and sequencing of the genes of
 RT betta-D-glucosyl-HMC-alpha-D-glucosyl-transferases of bacteriophages T2
 RT and T6.";
 RT Nucleic Acids Res. 21:1500-1504(1993).
 CC -1 - FUNCTION: TRANSFERS A GEMNTOBOSYL-GROUP ON AN
 CC HYDROXYMETHYLCYTOSINE RESIDUE IN DNA.
 CC -1 - PATHWAY: INVOLVED IN THE DNA MODIFICATION PROCESS TO PROTECTS
 CC THE PHAGE GENOME AGAINST ITS OWN NUCLEASES AND THE HOST
 CC RESTRICTION ENDONUCLEASE SYSTEM.
 CC -----
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 DR PIR; S35626; S35626.
 DR NCBI_TaxID=10664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93219141; PubMed=8464751;
 RA Winkler M., Rueger W.;
 RT "Cloning and sequencing of the genes of
 RT betta-D-glucosyl-HMC-alpha-D-glucosyl-transferases of bacteriophages T2
 RT and T6.";
 RT Nucleic Acids Res. 21:1500-1504(1993).
 CC -1 - FUNCTION: TRANSFERS A GEMNTOBOSYL-GROUP ON AN
 CC HYDROXYMETHYLCYTOSINE RESIDUE IN DNA.
 CC -1 - PATHWAY: INVOLVED IN THE DNA MODIFICATION PROCESS TO PROTECTS
 CC THE PHAGE GENOME AGAINST ITS OWN NUCLEASES AND THE HOST
 CC RESTRICTION ENDONUCLEASE SYSTEM.
 CC -----
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 DR PIR; S35626; S35626.
 DR NCBI_TaxID=10664;

SQ SEQUENCE 280 AA; 32299 MW; 44AA14226265BBDE CRC64;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-9800875; PubMed-9344866;
 RA Sawdargo M., George S.R., Nguyen T., Xu S., Kolakowski L.F. Jr.,
 RA O'Dowd B.F.;
 RT "A cluster of four novel human G protein-coupled receptor genes
 occurring in close proximity to CD22 gene on chromosome 19q13.1."
 RT Biochem. Biophys. Res. Commun. 239:543-547(1997).
 RL
 CC -!- FUNCTION: ORPHAN RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 DR EML; AF024687; AAB86710.1; -.
 DR Genew; HGNC:4498; GPR40.
 DR MIM; 603820; -.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_FL_1; FALSE_NEG.
 DR PROSTE; PS50267; G-PROTEIN_RECEP_FL_2; 1.
 KW PROSTE; PS50267; G-PROTEIN_RECEP_FL_1; FALSE_NEG.
 DR PROSTE; PS50267; G-PROTEIN_RECEP_FL_2; 1.
 DR PROSTE; PS50267; G-PROTEIN_RECEP_FL_1; FALSE_NEG.
 FT DOMAIN 1 10 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 11 31 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 42 CYTOPLASMIC.
 FT TRANSMEM 43 63 2 (POTENTIAL).
 CC PROTEIN OF THE MALONATE DECARBOXYLASE.
 CC -!- CATALYTIC ACTIVITY: Depospho-CoA + ATP = 2-(5'-
 CC triphosphoribosyl)-3'-dephospho-CoA + adenine.
 CC -!- SIMILARITY: BELONGS TO THE CITG/MDCB FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AD017138; BA036205.1; ALT_INIT.
 DR InterPro; IPR002756; CITG.
 DR Pfam; PF01874; CITG; 1.
 KW Lyase.
 SQ SEQUENCE 280 AA; 29150 MW; F43340A7DED9754D CRC64;
 QY 1 HARL 4
 DR Query Match 100.0%; Score 21; DB 1; Length 280;
 DR Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 DR Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR
 QY 1 HARL 4
 DR Query Match 100.0%; Score 21; DB 1; Length 300;
 DR Best Local Similarity 100.0%; Pred. No. 2e+02;
 DR Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR
 QY 1 HARL 4
 DR Query Match 100.0%; Score 21; DB 1; Length 300;
 DR Best Local Similarity 100.0%; Pred. No. 2e+02;
 DR Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR
 RESULT 44
 GPR_HUMAN STANDARD; PRT; 300 AA.
 ID GPR_HUMAN
 AC MMSR_PSEAE
 ID MMSR_PSEAE
 AC P28809;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE MMSR operon regulatory protein.
 GN GPR40;
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OC NCBI_TAXID=287;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 15692 / PAO1;
 RX MEDLINE=92317087; PubMed=1339433;
 RA Steele M.J., Lorenz D., Hatter A., Park A., Sokatch J.R.;
 RT "Characterization of the mmsAB operon of *Pseudomonas aeruginosa* PAO
 encoding methylmalonate-semialdehyde dehydrogenase and 3-
 hydroxyisobutyrate dehydrogenase.";
 RT RL J. Biol. Chem. 267:13585-13592(1992).
 RN [2] BioL. Chem. 267:13585-13592(1992).
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PAO1;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
 Ricker M.J., Brinkman F.S.L., Hufnagle W.O., Kowalki D.J., Lagrou M.,
 Garber R.L., Goitry L., Tolentino E., Westbroek-Wadman S., Yuan Y.,
 Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 Smith K.A., Spencer D.H., Wong G.K., Wu Z., Paulsen I.T.,
 Reizer J., Sauer M.H., Hancock R.E.W., Iory S., Olson M.V.,
 RT "Complete genome of *Pseudomonas aeruginosa* PAO1, an
 opportunistic pathogen.";
 RT Nature 406:959-964(2000).
 CC -I- FUNCTION: REGULATORY PROTEIN FOR THE MMSAB OPERON. ACTIVATES THE
 TRANSCRIPTION OF THE MSSAB GENES.
 CC -I- SIMILARITY: BELONGS TO THE ARAC/XYLS FAMILY OF TRANSCRIPTIONAL
 REGULATORS.
 CC -----
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 CC -----
 EMBL: M84911; AAA25890.1; -.
 DR PIR: AE004778; AA0G0959.1; -.
 DR PIR: S27601; S27601.
 DR PIR: A42902; A42902.
 DR Interpro; IPR000005; HTH_ARAC.
 DR Pfam; PF00165; HTH_ARAC; 2.
 DR PRINTS; PR00032; HTHARAC.
 DR SMART; SM00342; HTH_ARAC; 1.
 DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
 DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
 KW Transcription regulation; DNA-binding; Activator; Complete proteome.
 FT DNA_BIND 217 236 H-T-H MOTIF (BY SIMILARITY).
 FT CONFLICT 129 129 S -> T (IN REF. 1).
 SQ SEQUENCE 307 AA; 35379 MW; 9BF7AE348FAFD45 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 307;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Oy |||||
 Db 212 HARL 215

 RESULT 46
 MAL3_SCHPO STANDARD; PRT; 308 AA.
 ID MAL3_SCHPO STANDARD; PRT; 308 AA.
 AC 010113;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Microtubule integrity protein mal3.
 GN MAL3 OR SPAC18G6.15.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC NCBI_TaxID=4896;
 RN [1] SEQUENCE FROM N.A.

 RX MEDLINE=98012204; PubMed=9348288;
 RA Beinhauer J.D., Hagan T.M., Heermann J.H., Fleig U.;
 RT "Mal3, the fission yeast homologue of the human APC-interacting
 protein EB-1 is required for microtubule integrity and the
 maintenance of cell form.";
 RT RL J. Cell Biol. 139:717-728(1997).
 J. Cell Biol. 139:717-728(1997).
 J. Cell Biol. 139:717-728(1997).
 RL -----
 RN [2] SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feitell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodges G.,
 RA Holroyd S., Hornsby T., Howarth S., Jaggard K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall J., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitz E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp P.,
 RA Shelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Wolckaert G., Aert R., Robben J., Grymonprez B.,
 RA Welteveld J., Vandesteene E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzsche C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Egger P., Zimmermann W., Weidler H., Wambutt R., Punelle B.,
 RA Gorfeau A., Cadieu E., Dreano S., Gloux S., Lejaune V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gailhard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT -----
 RL Nature 415:871-880(2002).
 CC -I- FUNCTION: MAY PLAY A ROLE IN REGULATING THE INTEGRITY OF
 CC MICROTUBULES POSSIBLY BY INFLUENCING THEIR STABILITY.
 CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC; ASSOCIATED WITH MICROTUBULES.
 CC -I- SIMILARITY: TO YEAST BIM1.
 CC -----
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 CC -----
 DR EMBL; Y09518; CAA70707.1; -.
 DR EMBL; 26818; CAM92392.1; -.
 DR Interpro; IPR004953; EBL1.
 DR Pfam; PR03271; EBL1; 1.
 DR -----
 KW Microtubules
 SQ SEQUENCE 308 AA; 35094 MW; 9527D31CAA024256 CRC64;
 Query Match 100.0%; Score 21; DB 1; Length 308;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HARL 4
 Oy |||||
 Db 292 HARL 295

 RESULT 47
 MIAA_STRCO STANDARD; PRT; 312 AA.
 ID MIAA_STRCO STANDARD; PRT; 312 AA.
 AC 069967;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (IPP)

RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=97251357; PubMed=9097039;

RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,

RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,

RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,

RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,

RA Oshima T., Saito G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,

RA Yamamoto Y., Horiuchi T.;

RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";

RL DNA Res. 3:363-377(1996).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=97061202; PubMed=8905232;

RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,

RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,

RA Kimura S., Kitagawa M., Makino K., Masuda S., Mikl T., Mizobuchi K.,

RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y.,

RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,

RA Yano M., Horiuchi T.;

RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";

RL DNA Res. 3:137-155(1996).

CC -----
 CC -1. SIMILARITY: BELONGS TO THE UPF0028 (SWS) FAMILY.

CC -----
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CC -----
 CC DR EMBL; AE001810; AAD36776.1; -.

CC DR PIR; TM1709; -.

CC DR InterPro; IPR002882; UPF0052.

CC DR Pfam; PP01933; UPF0052; 1.

CC DR PIR; B36871; B36871.

CC DR ECOGene; EG12120; YcIK.

CC DR InterPro; IPR002541; Patatin.

CC DR InterPro; IPR001423; UPF0028.

CC DR Pfam; PF01734; Patatin; 1.

CC DR PROSITE; PS01237; UPF0028; 1.

CC KW HYPOTHETICAL PROTEIN; Complete proteome.

CC SQ SEQUENCE 314 AA; 34632 MW; 886FBEB17F3E06F44 CRC64;

CC Query Match 100.0%; Score 21; DB 1; Length 314;

CC Best Local Similarity 100.0%; Pred. No. 2.1e+02;

CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 HARL 4
 Db 126 HARL 129

Search completed: November 13, 2002, 13:41:17
 Job time : 11 secs

RESULT 50
 YH09_THEME STANDARD; PRT; 314 AA.
 ID YH09_THEME
 AC 09X235;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein TM1709.
 GN TM1709.
 OS Thermotoga maritima.

Qy 1 HARL 4
 Db 223 HARL 226

OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;

OC Thermotogaceae; Thermotoga.

NCBI_TaxID=2336;

[1]

SEQUENCE FROM N.A.

RC STRAIN=MSB8 / DSM 3109;

RX MEDLINE=99287316; PubMed=10360571;

RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.M.,

RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

RA Heidelberg J., Burton G.G., Fleischmann R.D., Eisen J.A., White O.,

RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,

RT Evidence for lateral gene transfer between Archaea and Bacteria from

RT genome sequence of Thermotoga maritima.";

RL Nature 399:23-32(1999).

CC -----
 CC -1. SIMILARITY: BELONGS TO THE UPF0052 FAMILY.

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CC -----
 CC DR EMBL; AE001810; AAD36776.1; -.

CC DR PIR; TM1709; -.

CC DR InterPro; IPR002882; UPF0052.

CC DR Pfam; PP01933; UPF0052; 1.

CC DR PIR; B36871; B36871.

CC DR ECOGene; EG12120; YcIK.

CC DR InterPro; IPR002541; Patatin.

CC DR InterPro; IPR001423; UPF0028.

CC DR Pfam; PF01734; Patatin; 1.

CC DR PROSITE; PS01237; UPF0028; 1.

CC KW HYPOTHETICAL PROTEIN; Complete proteome.

CC SQ SEQUENCE 314 AA; 34632 MW; 886FBEB17F3E06F44 CRC64;

CC Query Match 100.0%; Score 21; DB 1; Length 314;

CC Best Local Similarity 100.0%; Pred. No. 2.1e+02;

CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 HARL 4
 Db 126 HARL 129

Copyright (c) 1993 - 2002 Compugen Ltd.	GenCore version 5.1.3			
Run on:	November 13, 2002, 13:39:48 ; Search time 29 Seconds (without alignments) 28.420 Million cell updates/sec			
Title:	US-09-697-590-2_COPY_292_295			
Perfect score:	21			
Sequence:	1 HARL 4			
Scoring table:	BLOSUM62			
Searched:	Gapop 10.0 , Gapext 0.5			
Post-processing:	Minimum Match 0% Maximum Match 100%			
Database :	SPTRIMBL_21: 1: sp_archea: * 2: sp_bacteria: * 3: sp_fungi: * 4: sp_human: * 5: sp_invertebrate: * 6: sp_mammal: * 7: sp_nuc: * 8: sp_organelle: * 9: sp_phage: * 10: sp_plant: * 11: sp_ratodent: * 12: sp_virus: * 13: sp_vertebrate: * 14: sp_unclassified: * 15: sp_rvirus: * 16: sp_bacteriap: * 17: sp_archeap: *			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	31	2 Q9F115
2	21	100.0	37	4 Q9BQ22
3	21	100.0	39	12 Q9IW57
4	21	100.0	42	10 Q9S083
5	21	100.0	44	16 Q8U546
6	21	100.0	45	16 Q8Y1N1
7	21	100.0	52	5 Q97152
8	21	100.0	57	16 Q8XU79
9	21	100.0	59	17 Q27782
10	21	100.0	65	2 Q07026
11	21	100.0	67	16 Q8UJ23
12	21	100.0	68	12 Q8VAB5
13	21	100.0	69	4 Q9BU94
14	21	100.0	69	12 Q9YP21
15	21	100.0	70	10 Q943U1
16	21	100.0	74	12 Q9IK63
ALIGNMENTS				
RESULT 1				
ID: Q9F115	PRELIMINARY;	PRT;	31 AA.	
AC: Q9F115;				
DT: 01-MAR-2001 (TREMBLrel. 16, Created)				
DT: 01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT: 01-MAR-2001 (TREMBLrel. 16, Last annotation update)				
DE: Hypothetical 3.5 kDa protein.				
GN: EP0010.				
OS: Enterococcus faecalis (streptococcus faecalis).				
OC: Plasmid PAM373.				
OC: Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales; OC: Enterococcaceae; Enterococcus.				
OC: NCBI_TaxID:1351;				
RN: [1]				
RP: SEQUENCE FROM N.A.				
RX: MEDLINE=20453452; PubMed=10998166;				
RA: De Boever E.H., Clewell D.B., Fraser C.M.:				
RT: "Enterococcus faecalis conjugative plasmid PAM373: complete nucleotide sequence and genetic analyses of sex pheromone response.",				
RL: Mol. Microbiol. 37:1327-1341(2000).				
DR: EMBL; AE005565; AAG40421; -				
KW: Hypothetical protein; Plasmid.				
SQ: SEQUENCE 31 AA; 3509 MW; 4E19CB94B3DB9421 CRC64;				
RESULT 2				
QY	1 HARL 4			
DB	12 HARL 15			
RESULT 2				
Q9BQ22	ID: Q9BQ22	PRELIMINARY;	PRT;	
AC: Q9BQ22;				
DT: 01-JUN-2001 (TREMBLrel. 17, Created)				

DT 01-JUN-2001 (TREMBLrel. 17; last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20; last annotation update)
 DE Alpha-2-macroglobulin (Fragment).
 GN A2M.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Teich N., Mossner J., Keim V.;
 RT "Coding sequence of alpha-2-macroglobulin exon 18 and flanking
 introns";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Teich N., Mossner J.J., Keim V.;
 RT "Homo sapiens alpha-2-macroglobulin (A2M), exon 18, A2M-2 allele.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF346032; AAK38109.1; -;
 DR InterPro; IPR01593; MacroglobinA2.
 DR Pfam; PF02027; A2M; 1.
 FT NON_TER 1
 FT 37 37
 SQ SEQUENCE 37 AA; 4390 MW; AFE1C0124ACBF415 CRC64;

Query Match 100.0%; Score 21; DB 4; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 8 HARL 11

RESULT 3
 Q9IW57 PRELIMINARY; PRT; 39 AA.
 ID Q9IW57;
 AC 09IW57;
 DT 01-OCT-2000 (TREMBLrel. 15; Created)
 DT 01-OCT-2000 (TREMBLrel. 15; Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16; Last annotation update)
 DE Glycoprotein (Fragment).
 GN GP57.
 OS Bornavirus (BDV).
 OC viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
 OC Bornavirus;
 OC NCBITaxID=12455;
 RN [1]
 RP SEQUENCE FROM N.A.
 STRAIN=RATBDBV;
 MEDLINE=20086018; PubMed=10622306;
 RA Schmeimle M., Jehle C., Formella S., Staeheli P.;
 RT "Sequence similarities between human Bornavirus isolates and
 laboratory strains question their human origin.";
 RL Lancet 354:1973-1974(1999);
 EMBL; AJ250179; CAB87242.1; -
 FT NON_TER 39
 SQ SEQUENCE 39 AA; 4205 MW; D5A828BD9C28FL134 CRC64;

Query Match 100.0%; Score 21; DB 12; Length 39;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 4 HARL 7

RESULT 4
 Q9SQ83 PRELIMINARY; PRT; 42 AA.
 ID Q9SQ83;

RESULT 5
 Q8U546 PRELIMINARY; PRT; 44 AA.
 ID Q8U546;
 AC 08U546;
 DT 01-JUN-2002 (TREMBLrel. 21; Created)
 DT 01-JUN-2002 (TREMBLrel. 21; Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21; Last annotation update)
 DE AGR_C_4298P.
 GN AGR_C_4298.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobium; Rhizobiaceae; Rhizobium.
 OX NCBITaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=21608551; PubMed=11743194;
 RX Gooden B., Hinke G., Gartung S., Miller N., Blanchard M., Mullin L.,
 RA Quollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Boumiel K., Gordon J., Vaudin M., Hartchouk O., Epp A., Liu F.,
 RA Wollan C., Allinger M., Dougherty D., Scott C., Lappas C., Marrelz B.,
 RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slatier S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58.";
 RT Agrobacterium tumefaciens C58.;
 RL Science 294:2323-2328(2001).
 EMBL; AE008151; AAK88107.1; -
 SQ SEQUENCE 44 AA; 4868 MW; B29035AD358B6A8C CRC64;

Query Match 100.0%; Score 21; DB 16; Length 44;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HARL 4
 Db 12 HARL 15

RESULT 6

08YIN1	PRELIMINARY;	PRT;	45 AA.
ID			
AC			
DT	01-MAR-2002 (TREMBrel. 20, Last sequence update)		
DT	01-MAR-2002 (TREMBrel. 20, Last annotation update)		
DE	Putative Pilin protein.		
GN	RSC0659 OR RS0156.		
OS	Ralstonia solanacearum (Pseudomonas solanacearum).		
OC	Bacteria; Proteobacteria; beta subdivision; Ralstonia group;		
OC	Ralstonia.		
OX	NCBI_TaxID=305;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=GM11000;		
RX	MEDLINE=21681879; PubMed=11823852;		
RA	Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,		
RA	Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,		
RA	Chandler M., Choisne N., Claude-Renard C., Cunnac S., Demange N.,		
RA	Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schliex T.,		
RA	Siglier P., Thebaud P., Whalen M., Wincker P., Levy M.,		
RA	Weissenbach J., Boucher C.A.;		
RT	"Genome sequence of the plant pathogen Ralstonia solanacearum.";		
RL	Nature 415:497-502(2002).		
DR	EMBL; AL646060; CAD14189.1; -		
KW	Complete proteome.		
SQ	SEQUENCE 45 AA; 4776 MW; 9C76F7F9D65B3F05 CRC64;		

Query Match 100.0%; Score 21; DB 16; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 HARL 4
Db 12 HARL 15

RESULT 7

091152	PRELIMINARY;	PRT;	52 AA.
ID			
AC			
DT	01-MAY-1999 (TREMBrel. 10, Last sequence update)		
DT	01-JUN-2001 (TREMBrel. 17, Last annotation update)		
DE	Reverse transcriptase (Fragment).		
GN	R1-ELEMENT\POL.		
OS	Drosophila arizona (Fruit fly).		
OC	Euryptera; Metazoa; Arthropoda; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydriidae; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7363;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Tovar F.J., Rodarte S.R., Almeida R.C., Leoncini O.;		
RT	"R1 element in Drosophila arizona.",		
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AR14256; ADU18018.1; -		
DR	FlyBase; FBgn0043769; Dari\RI-element\pol.		
DR	RNA-directed DNA Polymerase.		
FT	NON_TER 1		
FT	NON_TER 52		
SQ	SEQUENCE 52 AA; 6215 MW; B511A4FC41B2A40A CRC64;		
Qy	Query Match 100.0%; Score 21; DB 5; Length 52;		
Qy	Best Local Similarity 100.0%; Pred. No. 3.1e+02;		
Qy	Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Db	1 HARL 4		
Db	26 HARL 29		

RESULT 8

08XUV9	PRELIMINARY;	PRT;	57 AA.
ID			
AC			
DT	01-MAR-2002 (TREMBrel. 20, Created)		
DT	01-MAR-2002 (TREMBrel. 20, Last sequence update)		
DT	01-MAR-2002 (TREMBrel. 20, Last annotation update)		
DE	Hypothetical protein RSC3074.		
GN	RSC3074 OR RS00523.		
OS	Ralstonia solanacearum (Pseudomonas solanacearum).		
OC	Bacteria; Proteobacteria; beta subdivision; Ralstonia group;		
OC	Ralstonia.		
OX	NCBI_TaxID=305;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=GM11000;		
RX	MEDLINE=21681879; PubMed=11823852;		
RA	Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,		
RA	Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,		
RA	Chandler M., Choisne N., Claude-Renard C., Cunnac S., Demange N.,		
RA	Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schliex T.,		
RA	Siglier P., Thebaud P., Whalen M., Wincker P., Levy M.,		
RA	Weissenbach J., Boucher C.A.;		
RT	"Genome sequence of the plant pathogen Ralstonia solanacearum.";		
RL	Nature 415:497-502(2002).		
DR	EMBL; AL646073; CAD16783.1; -		
KW	Hypothetical protein; Complete proteome.		
SQ	SEQUENCE 57 AA; 6465 MW; 034B748142BD2 CRC64;		

Query Match 100.0%; Score 21; DB 16; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 1 HARL 4
Db 39 HARL 42

RESULT 9

027782	PRELIMINARY;	PRT;	59 AA.
ID			
AC			
DT	027782; (TREMBrel. 05, Created)		
DT	01-JAN-1998 (TREMBrel. 05, Last sequence update)		
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)		
DE	Hypothetical protein MTH1750.		
GN	MTH1750.		
OS	Methanobacterium thermoautotrophicum.		
OC	Archaea; Euryarchaeota; Methanobacteriaceae; Methanothermobacter.		
OC	NCBI_TaxID=187420;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=DELTA_H;		
RX	MEDLINE=98037514; PubMed=9371463;		
RA	Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,		
RA	Aldridge T., Bashirudeen R., Blakely D., Cook R., Gilbert K.,		
RA	Harrison D., Hoang L., Keagle P., Lumm W., Portier B., Qiu D.,		
RA	Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,		
RA	Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,		
RA	McDonald S., Shimer G., Goyal A., Pietrovski S., Church G.M.,		
RA	Daniel C.J., Mao J.-I., Rice P., Noelting J., Reeve J.N.,		
RA	"Complete genome sequence of Methanobacterium thermoautotrophicum J. Bacteriol. 179:1135-1155(1997)."		
RA	EMBL; AE000930; AAB66220.1; -		
DR	InterPro: IPR004820; CytidylLytransf.		
DR	Pfam: PF01467; CytidylLytransf; 1.		
KW	Hypothetical protein; Complete proteome.		
SQ	SEQUENCE 59 AA; 6658 MW; 6559DB37EED72FO CRC64;		

Qy	1 HARL 4		RA	Nester E.W.;
			RT	"The genome of the natural genetic engineer Agrobacterium tumefaciens C58";
ID	15 HARL 18		RT	Science 294:2317-2323(2001).
Db			RL	EMBL; AE008985; AAI41140.1; -.
			DR	HYPOTHETICAL PROTEIN; Complete Proteome.
			KW	SEQUENCE 67 AA; 7608 MW; 351679E2DBB08499 CRC64;
			SQ	
RESULT 10			Query Match	100.0%; Score 21; DB 17; Length 59;
007026			Best Local Similarity	100.0%; Pred. No. 3.9e+02; Mismatches 0;
ID	007026	PRELIMINARY;	Indels	0; Gaps 0;
AC	007026;			
DT	01-NOV-1996 (TREMBrel. 01, Last sequence update)			
DT	01-NOV-1998 (TREMBrel. 08, Last annotation update)			
DE	RFBQ protein.			
GN	RFBQ.			
OS	Vibrio cholerae.			
OC	Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.			
OX	NCBI_TaxID=666;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=O17 / BIOTYPE EL TOR / SEROTYPE OGAWA;			
RX	MEDLINE=92212870; PubMed=1372980;			
RA	Stroehner U.H., Karageorgos L.E., Morona R., Manning P.A.;			
RT	"Putative O-antigen transport genes within the rfb region of Vibrio			
RT	cholerae O1 are homologous to those for capsule transport.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2566-2570(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=O17 / BIOTYPE EL TOR / SEROTYPE OGAWA;			
RX	MEDLINE=95309704; PubMed=7540582;			
RA	Manning P.A., Stroehner U.H., Karageorgos L.E., Morona R.;			
RT	"Putative O-antigen transport genes within the rfb region of Vibrio			
RT	cholerae O1 are homologous to those for capsule transport.";			
RL	Gene 158:1-7(1995).			
DR	EMBL: X59554; CAA42147.1; -.			
RX	SEQUENCE 65 AA; 7577 MW; 59FA6094E6686E544 CRC64;			
RA				
RT	Best Local Similarity 100.0%; Pred. No. 3.8e+02; Length 65;			
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 HARL 4		RESULT 12	
			08VAB5	
ID	08VAB5	PRELIMINARY;	ID	08VAB5
AC	08VAB5;		PRT;	68 AA.
DT	01-MAR-2002 (TREMBrel. 20, Created)			
DT	01-MAR-2002 (TREMBrel. 20, Last sequence update)			
DE	WSV511 (WSSV037).			
OS	White spot syndrome virus (WSSV).			
OC	Viruses; unclassified viruses.			
OX	NCBI_TaxID=92652;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21548311; PubMed=11689662;			
RA	Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;			
RT	"Complete genome sequence of the shrimp white spot bacilliform			
RT	virus.";			
RL	J. Virol. 75:11811-11820(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=TAIWAN;			
RX	MEDLINE=20517548; PubMed=11062040;			
RA	Tsai M.F., Yu H.T., Teng H.F., Leu J.H., Chou C.M., Huang C.J.,			
RA	Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;			
RT	"Identification and characterization of a shrimp white spot syndrome			
RT	virus (WSSV) gene that encodes a novel chimeric polypeptide of			
RT	cellular-type thymidine kinase and thymidylate kinase";			
RL	virology 277:100-110(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=TAIWAN;			
RX	MEDLINE=21844071; PubMed=11653398;			
RA	Chen L.I., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,			
RA	Lo C.F., Kou G.H.;			
RT	"Identification of a nucleocapsid protein (VP35) gene of shrimp white			
RT	spot syndrome virus and characterization of the motif important for			
RT	targeting VP35 to the nuclei of transfected insect cells.";			
RL	Virology 293:44-53(2002).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=TAIWAN;			
RA	Kou G.-H.;			
RA	Submitted (Oct-2001) to the EMBL/GenBank/DDJB databases.			
DR	EMBL; AF332093; AAL3352.1; -.			
DR	EMBL; AF440805.1; -.			
SQ	SEQUENCE 68 AA; 8104 MW; 61908AE8049D14D CRC64;			
Query Match	100.0%; Score 21; DB 12; Length 68;			
Best Local Similarity	100.0%; Pred. No. 4e+02; Mismatches 0;			
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 HARL 4			

RESULT 24	Q9K5X7	PRELIMINARY;	PRT;	83 AA.
ID	Q9K5X7;			
AC				
DT	01-OCT-2000 (TREMBrel. 15, Created)			
DT	01-OCT-2000 (TREMBrel. 15, Last sequence update)			
FT	01-MAR-2002 (TREMBrel. 20, Last annotation update)			
DE	Hypothetical protein BH3959.			
GN	BH3959.			
OS	Bacillus halodurans			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;			
OC	Bacillaceae; Bacillus.			
OX	NCBI_TaxID=86665;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C-125 / JCM 9153;			
RX	MEDLINE=00512582; PubMed=11050132;			
RA	Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,			
RA	Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,			
RA	Horiuchi K.;			
RT	"Complete genome sequence of the alkaliphilic bacterium <i>Bacillus halodurans</i> and genomic sequence comparison with <i>Bacillus subtilis</i> ."			
RL	Nucleic Acids Res. 28:4317-4331(2000).			
DR	EMBL: AP001520; BAM07678.1; -			
KW	Hypothetical protein; Complete proteome;			
SQ	SEQUENCE 83 AA; 9977 MW; 1EE8407781B52C20 CRC64;			
Query Match	100.0%	Score 21; DB 16; Length 83;		
Best Local Similarity	100.0%	Pred. No. 4.9e+02;		
Matches	4;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 HARL 4			
Db	35 HARL 38			
RESULT 25				
Q66074	PRELIMINARY;	PRT;	85 AA.	
ID	Q66074;			
AC				
DT	01-NOV-1996 (TREMBrel. 01, Created)			
DT	01-NOV-1996 (TREMBrel. 01, Last sequence update)			
FT	01-DEC-2001 (TREMBrel. 19, Last annotation update)			
DE	Virion protein (Fragment).			
OS	Canine herpesvirus.			
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			
OC	Alphaherpesvirinae;			
OC	Alphaherpesvirinae;			
OX	NCBI_TaxID=37110;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21608551; PubMed=11743194;			
RA	Goodner B., Hinne G., Gattung S., Miller N., Blanchard M., Mullin L.,			
RA	Ourolo B., Goldman B. S., Cao Y., Askenazi M., Halling C., Mullin L.,			
RA	Houmeli K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,			
RA	Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markliz B.,			
RA	Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,			
RA	Cielo C., Slater S.;			
RT	"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."			
RT	Science 294:2323-2326(2001).			
RL	Science 294:2323-2326(2001).			
DR	EMBL: AE000008; AAL41398.1; -			
DR	EMBL: AE007975; AAK86193.1; -			
KW	Hypothetical protein; Complete Proteome;			
SQ	SEQUENCE 85 AA; 9466 MW; 51BB33B66A33219 CRC64;			
Query Match	100.0%	Score 21; DB 16; Length 85;		
Best Local Similarity	100.0%	Pred. No. 4.9e+02;		
Matches	4;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 HARL 4			
Db	7 HARL 10			
RESULT 27				
O9FD17	PRELIMINARY;	PRT;	87 AA.	
ID	O9FD17;			
AC	O9FD17;			
DT	01-MAR-2001 (TREMBrel. 16, Created)			
DT	01-MAR-2001 (TREMBrel. 16, Last sequence update)			
FT	01-JUN-2002 (TREMBrel. 21, Last annotation update)			
DE	Acyl carrier protein.			
GN	RUBC			
OS	Streptomyces collinus.			
OC	Bacteria; Firmicutes; Actinobacteridae;			
OC	Actinomycetidae; Streptomyceinae; Streptomyctaceae; Streptomyces.			
OX	NCBI_TaxID=42684;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=DSM2012;			

RA	Martin R., Bailey J.E., Minas W;	OX	NCBI_TAXID=83229;
RT	"Rubromycin Polyketide synthase from Streptomyces collinus DSM2012. ";	RN	[1]
RL	Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.	RP	SEQUENCE FROM N.A.
DR	EMBL; AF293355; AAG03069.1; -	RA	Peterschmitt M., Granier M., Aboulama S.;
DR	HSSP; Q02054; 2AF8;	DR	"First report of tomato yellow leaf curl Geminivirus virus in
DR	InterPro; IPR003880; Ppantne_attach.	RT	MOROCCO. "
DR	Pfam; PF00550; PP-binding; 1;	RL	Plant Dis. 83: 1074-1074 (1999).
DR	PROSITE; PS5075; ACP_DOMAIN; 1;	DR	EMBL; AU133491; CAB38575.1; -
DR	PROSITE; PS00012; PHOSPHOPANTETHINE; UNKNOWN_1.	DR	InterPro; IPR002511; Gemini_VI.
KW	Phosphopantetheine.	DR	Pfam; PF01524; Gemini_VI; 1.
SQ	SEQUENCE 87 AA; 9792 MW; 235B0DC875F14C0 CRC64;	DR	Prodrom; PD005978; Gemini_VI; 1.
Qy	Query Match 100.0%; Score 21; DB 2; Length 87; Best Local Similarity 100.0%; Pred. No. 5e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	KW	Cool protein
Db	Db 79 HARL 82	SQ	SEQUENCE 88 AA; 10378 MW; 32D149F7EB0FF9C39 CRC64;
RESULT 28		Qy	Query Match 100.0%; Score 21; DB 12; Length 88; Best Local Similarity 100.0%; Pred. No. 5e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q9FB23	PRELIMINARY; ID 09FB23	Db	Db 65 HARL 68
AC	09FB23; STRAIN="A(3(2)) / M145;"	Q9FB23	PRELIMINARY; PRT; 87 AA.
DT	01-MAR-2001 (TREMBLrel. 16, Created)	ID	Q93SB6
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	Q93SB6	PRELIMINARY; PRT; 92 AA.
DE	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	AC	Q93SB6;
DE	Hypothetical protein SC07189.	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
GN	SC07189 OR SC8411.17C.	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
OS	Streptomyces coelicolor.	DE	Hypothetical 10.1 kDa protein.
OC	Bacteria; Firmicutes; Actinobacteridae;	OS	Frankia sp. Ari13.
OC	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.	OC	Plasmid pFO31.
OX	NCBI_TaxID=1902;	OC	Bacteria; Firmicutes; Actinobacteridae;
RN	[1] SEQUENCE FROM N.A.	OX	Actinomycetales; Frankineae; Frankiaceae; Frankia.
RC	STRAIN="A(3(2)) / M145;"	RN	NCBI_TaxID=1858;
RA	Bentley S.D., Chatter K.F., Cerdeno-Tarrega A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Harke L., Murphy L., Oliver K., O'Neill S., Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Taylor K., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J., Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";	RP	[1] SEQUENCE FROM N.A.
RT	Nature 417:141-147 (2002).	RC	STRAIN=A(3(2);
DR	EMBL; AL331041; CAC01589.1; -.	RX	MEDLINE-21184415; PubMed=11287155;
KW	Hypothetical protein.	RA	Leavire C., Louis D., Perriere G., Briolay J., Normand P., Cournoyer B.; "Analysis of pFO31, a 8551-bp cryptic plasmid from the symbiotic nitrogen-fixing actinomycete Frankia.;"
SQ	SEQUENCE 87 AA; 9955 MW; F0008D1049B11D4B CRC64;	RT	FEMS Microbiol. Lett. 197:111-116 (2001).
Qy	Query Match 100.0%; Score 21; DB 16; Length 87; Best Local Similarity 100.0%; Pred. No. 5e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	EMBL; AU29745; CAC39461.1; -.
Db	Db 41 HARL 44	KW	Hypothetical protein; Plasmid.
RESULT 29		Qy	Query Match 100.0%; Score 21; DB 2; Length 92; Best Local Similarity 100.0%; Pred. No. 5.2e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
O9YKDS	PRELIMINARY; ID 09YKDS	Db	Db 24 HARL 27
AC	O9YKDS; 01-MAY-1999 (TREMBLrel. 10, Created)	RESULT 31	
AC	01-MAY-1999 (TREMBLrel. 10, Last sequence update)	ID	Q18842
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)	Q18842	PRELIMINARY; PRT; 93 AA.
DT	01-NOV-1996 (TREMBLrel. 01, Created)	AC	Q18842;
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
AC	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	C54G10_1 protein.	DE	C54G10_1.
GN	V2.	OS	Caenorhabditis elegans.
OS	tomato yellow leaf curl virus - II.	OC	Eukaryota; Metazoa; Nemataoda; Chromadorea; Rhabditida; Rhabditoidae;
OC	Viruses; ssDNA viruses; Geminiviridae; Begomovirus.	OC	Rhabditidae; Peioderinae; Caenorhabditis.
RN	[1] SEQUENCE FROM N.A.	OX	NCBITaxID=6239;
RP		RN	

RA Matthews L.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP
 RX
 RA
 RT "Genome sequence of the nematode *C.elegans*: A platform for investigating biology.";
 RL Science;82:2012-2018(1998).
 DR EMBL; Z75532; CAA9809.1; -.
 SQ SEQUENCE 93 AA; 10885 MW; C00F5DC1515DE15B CRC64;

Query Match 100.0%; Score 21; DB 5; Length 93;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4
 Db 19 HARL 22

RESULT 32
 091113 PRELIMINARY; PRT; 93 AA.
 ID 091113
 AC 091113
 DT 01-MAR-2001 (TREMBrel. 16, Created)
 DT 01-MAR-2001 (TREMBrel. 16, Last sequence update)
 DT 01-OCT-2001 (TREMBrel. 18, Last annotation update)
 DE Hypothetical protein PA2292.
 GN PA2292.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TAXID=287;
 [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=ACC 15692 / PAOL;
 RX MEDLINE=20437337; PUBMED=10984043;
 RA Stover C.R., Pham X.Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
 RA Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalki D.J., Lagrou M.,
 RA Garber R.L., Goitry L., Tolentino E., Westbroek-Wadman S., Yuan Y.,
 RA Brody L.B., Coulter S.N., Folger K.A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAOL, an opportunistic pathogen.";
 RT Nature;406:959-964(2000).
 RL EMBL; AE00455; AAC0560.1;
 DR InterPro; IPR000886; ER target.
 DR PROSITE; PS00014; ER TARGET; UNKNOWN 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 93 AA; 10732 MW; A3854IEC2FI2AF22 CRC64;

Query Match 100.0%; Score 21; DB 16; Length 93;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4
 Db 31 HARL 34

RESULT 33
 08ZK19 PRELIMINARY; PRT; 95 AA.
 ID 08ZK19
 AC 08ZK19;
 DT 01-MAR-2002 (TREMBrel. 20, created)
 DT 01-MAR-2002 (TREMBrel. 20, last sequence update)
 DT 01-MAR-2002 (TREMBrel. 20, last annotation update)
 DE Putative integrase.
 GN STM488.
 OS *Salmonella typhimurium*. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC *Salmonella*.
 OC NCBI_TAXID=602;
 RN [1]
 RP
 RX SEQUENCE FROM N.A.
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RA MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
 RA RT "Complete genome sequence of *Salmonella enterica* serovar *Typhimurium* LT2.";
 RL Nature; 413:852-856(2001).
 DR EMBL; AE008910; AAL23306.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 95 AA; 10938 MW; 479F972FCCE1FDFFD CRC64;

Query Match 100.0%; Score 21; DB 16; Length 95;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4
 Db 10 HARL 13

RESULT 34
 038025 PRELIMINARY; PRT; 95 AA.
 ID 038025
 AC 038025;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE ORF 4.
 GN 4.
 OS Bacteriophage phi-C31.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC Lambda-like viruses.
 OX NCBI_TAXID=10719;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9434705; PUBMED=8088546;
 RA Hartley N.M., Murphy G.O., Bruton C.J., Chater K.F.;
 RT "Sequence of the essential early region of phi C31, a temperate phage of *Streptomyces* spp. with unusual features in its lytic development.";
 RT Gene 147:29-40(1994).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NORWICH STOCK;
 RA Smith M.C.M.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NORWICH STOCK;
 RX MEDLINE=99162580; PubMed=10051617;
 RA Hendrix R.W., Smith M.C.M., Burns N., Ford M.E., Hatfull G.F.;
 RT "Evolutionary relationships among diverse bacteriophages and prophages: all the world's a phage.";
 RT Proc. Natl. Acad. Sci. U.S.A. 96:2192-2197(1999).
 RL EMBL; X76288; CAA53915.1; -.
 DR EMBL; AJ006589; CAA07129.1; -.
 SQ SEQUENCE 96 AA; 10601 MW; 6C136673B5BB4E63 CRC64;

Query Match 100.0%; Score 21; DB 9; Length 96;
 Best Local Similarity 100.0%; Pred. No. 5.4e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HARL 4
 Db 82 HARL 85

RESULT 35				
ID Q9M9W0	PRELIMINARY;	PRT;	97 AA.	
AC Q9M9W0		AC;		
DT 01-OCT-2000 (TREMBrel. 15, Created)		DT;		
DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)		DT;		
DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)		DE;		
DE F18C1_18 protein.				
GN F18C1_18.				
OS Arabidopsis thaliana (Mouse-ear cress);				
OC Eukaryota; Viriplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;				
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
OX NCBI_TAXID=3702;				
RN [1]	SEQUENCE FROM N.A.			
RC STRAIN=CY. COLUMBIA;				
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,				
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,				
RA Bowman C.L., White O., Nieman W.C., Fraser C.M.;				
RT "Arabidopsis thaliana chromosome III BAC F18C1 genomic sequence.";				
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.				
DR EMBL; AC01620; ARK26142.1; -.				
SQ SEQUENCE 97 AA; 10967 MW; 3C45FBCE676327F9 CRC64;				
RESULT 36				
ID 087620	PRELIMINARY;	PRT;	99 AA.	
AC 087620;		PR		
DT 01-NOV-1998 (TREMBrel. 08, Created)				
DT 01-JUN-2002 (TREMBrel. 08, Last sequence update)				
DE O-halobenzoate dioxygenase ferredoxin.				
GN OHBD.				
OS Pseudomonas aeruginosa.				
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;				
OC Pseudomonas				
OX NCBI_TAXID=287;				
RN [1]	SEQUENCE FROM N.A.			
RC STRAIN=JB2;				
RC MEDLINE=21455015; PubMed=11571162;				
RA Hickey W.J., Sabat G., Yuroff A.S., Arment A.R., Perez-Lesher J.;				
RT "Cloning, Nucleotide Sequencing, and Functional Analysis of a Novel, Mobile Cluster of Biodegradation Genes from Pseudomonas aeruginosa Strain JB2.;"				
RL Appl. Environ. Microbiol. 67:4603-4609 (2001).				
DR HSSP; P37332; IPIOT;				
DR InterPro; IPR001281; Rieske.				
DR Pfam; PF00355; Rieske; 1.				
KW dioxygenase.				
SQ SEQUENCE 99 AA; 10836 MW; 07C198B76AF24EA3 CRC64;				
Query Match 100.0%; Score 21; DB 2; Length 99;				
Best Local Similarity 100.0%; Pred. No. 5.6e+02;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 1 HARL 4				
Db 43 HARL 46				
RESULT 37				
ID Q926Q7	PRELIMINARY;	PRT;	100 AA.	
AC Q926Q7;		AC;		
DT 01-DEC-2001 (TREMBrel. 19, Created)		DT;		
DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)		DT;		
DE Hypothetical protein RC1065.				
GN RC1065.				
OS Rickettsia conorii.				
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;				
OC Rickettsiaceae; Rickettsiae; Rickettsia.				
OX NCBI_TAXID=781;				
RN [1]	SEQUENCE FROM N.A.			
RC STRAIN=MALISH 7;				
RA Ogata H., Audit C.S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,				
RA Raoult D.; Roux V., Cossart P., Weissenbach J., Claverie J.-M., Samson D.;				
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";				
RL Science 293:1993-1998(2001).				
DR EMBL; AE00865; AAL03603.1; -.				
KW Hypothetical protein; Complete proteome.				
SQ SEQUENCE 100 AA; 11611 MW; D454112ACDAEL67 CRC64;				
Query Match 100.0%; Score 21; DB 16; Length 100;				
Best Local Similarity 100.0%; Pred. No. 5.6e+02;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 1 HARL 4				
Db 77 HARL 80				
RESULT 38				
ID Q93U17	PRELIMINARY;	PRT;	101 AA.	
AC Q93U17;		AC;		
DT 01-DEC-2001 (TREMBrel. 19, Created)		DT;		
DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)		DE;		
DE Reck (Fragment).				
GN RECA.				
OS Bacteroides ovatus.				
OC Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;				
OC Bacteroides.				
OX NCBI_TAXID=28116;				
RN [1]	SEQUENCE FROM N.A.			
RC STRAIN=FL120C;				
RA Gutacker M.M., Piffaretti J.-C.;				
RT "Sequence diversity within the recA and glnA genes of <i>B. fragilis</i> delineates two subgroups associated to different antibiotic resistance genotypes (cepA and cfIA)." ;				
RT Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.				
RL EMBL; AP280747; ARK4940.1; -.				
DR InterPro; IPR00153; RECA.				
DR Pfam; PF00154; RECA; 1.				
DR PRODOM; PD000229; RECA; 1.				
DR PROSITE; PS50162; RECA_2; 1.				
FT NON_TER 1				
FT NON_TER 101				
SQ SEQUENCE 101 AA; 11016 MW; BA418B0AD44211C2 CRC64;				
Query Match 100.0%; Score 21; DB 2; Length 101;				
Best Local Similarity 100.0%; Pred. No. 5.7e+02;				
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 1 HARL 4				
Db 74 HARL 77				

RESULT 39						
Q9JRG6	PRELIMINARY;	PRT;	101 AA.			
ID Q9JRG6;						
AC Q9JRG6;						
DT 01-OCT-2000 (TREMBrel. 15, Created)						
DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)						
DE HYPothetical protein NMA0377.						
GN NMA0377 OR NM_00377.						
OS Neisseria meningitidis (serogroup A), and						
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.						
OX NCBI_TaxID=65659;						
RA [1]						
RN Sequence FROM N.A.						
RP STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;						
RX MEDLINE=2022256; PubMed=10761919;						
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,						
RA Klie S.R., Morelli G., Basham D., Brown D., Chillingworth T., Hamlin N., Holroyd S.,						
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hailey J., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,						
RA Whitehead S., Spratt B.G., Barrell B.G.;						
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491";						
RT Nature 404:502-506(2000).						
RN [2]						
RP SEQUENCE FROM N.A.						
RC STRAIN=MCS8 / SEROGROUP B;						
RX MEDLINE=10715755; PubMed=10710307;						
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Pedersen J.F., Dodson R.J., Nelson W.C., Gwin M.L., Debey R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scariato V., Madignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;						
RA MC58;"						
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58";						
RL Science 287:1809-1815(2000).						
DR EMBL; AL162753; CAB8878.1; -.						
DR EMBL; AE002555; AAF42378.1; -.						
DR TIGR; NM_002058; -.						
KW Hypothetical protein; Complete proteome.						
SQ SEQUENCE 101 AA; 10908 MW; 18938C359C04FCB6 CRC64;						
Query Match Best Local Similarity 100.0%; Score 21; DB 16; Length 101; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
OY 1 HARL 4						
Db 12 HARL 15						
RESULT 40						
O37880 PRELIMINARY; PRT; 102 AA.						
ID 037880;						
AC 037880;						
DT 01-JAN-1998 (TREMBrel. 05, Created)						
DT 01-JAN-1998 (TREMBrel. 05, Last sequence update)						
DE VI protein (fragment).						
V1 Tomato yellow leaf curl virus - Israel.						
OS OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.						
NCBI_TaxID=66366;						
RA [1]						
RP SEQUENCE FROM N.A.						
RC STRAIN=SPAIN_S2697;						
RA Navas-Castillo J., Sanchez-Campos S., Diaz J.A., Saez-Alonso E., Moriones E.;						
RA Moriones E.;						
RA ...;						
RESULT 42						
OBUGL9 PRELIMINARY; PRT; 103 AA.						
ID OBUGL9						
AC OBUGL9;						
DT 01-JUN-2002 (TREMBrel. 21, Created)						
DT 01-JUN-2002 (TREMBrel. 21, Last sequence update)						
DE Hypothetical protein Atu1018.						
GN Atu1018 OR AGRC_1875						
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).						
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group.						
OX NCBI_TaxID=176295;						

RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=21608550; PubMed=11743193;						
RA	Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.-P.,						
RA	Oikura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,						
RA	Chen Y., Paulsen I.T., Eisen J.A., Kap P.D., Boyce D. Sr.,						
RA	Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,						
RA	Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,						
RA	Raymond C., Rose G., Saengkhammachak C., Wu Z., Romero P., Gordon D.,						
RA	Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,						
RA	Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,						
RA	Chunley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,						
RA	Nester B.W., C58. ;						
RT	"The genome of the natural genetic engineer Agrobacterium tumefaciens						
RL	Science 294:2317-2323(2001).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=21608551; PubMed=11743194;						
RA	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Halling C., Mullin L.,						
RA	Ourollo B., Goldman B.S., Cao Y., Aszkenasy M., Halling C., Mullin L.,						
RA	Houmeliel K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F.,						
RA	Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markezic B.,						
RA	Flanagan C., Crowell C., Ginson J., Lemo C., Sear C., Strub G.,						
RA	Cielo C., Slater S.,						
RT	"Genome sequence of the plant pathogen and biotechnology agent						
RT	Agrobacterium tumefaciens C58. ;						
RL	Science 294:2323-2328(2001).						
DR	EMBL; AE002066; AAC40311.1. ;						
DR	EMBL; AE008032; AAC86261.1. ;						
KW	Hypothetical protein; Complete proteome.						
SQ	SEQUENCE 103 AA; 11758 MW; C7F6B067D456E62A CRC64;						
Query Match	100.0%; Score 21; DB 16; Length 103;						
Best Local Similarity	100.0%; Pred. No. 5.8e+02;						
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
QY	1 HARL 4						
DB	61 HARL 64						
RESULT 43							
Q8USL6	PRELIMINARY; PRT; 103 AA.						
ID	Q8USL6;						
AC	Q8USL6; PRELIMINARY; PRT; 103 AA.						
DT	01-JUN-2002 (TREMBREL 21, Last sequence update)						
DT	01-JUN-2002 (TREMBREL 21, Last annotation update)						
DE	AGR_C_774.						
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970).						
OC	Bacteria; Proteobacteria; alpha subdivision: Rhizobiaceae group;						
OC	Bacteria; Proteobacteria; Rhizobiaceae; Rhizobium.						
OX	NCBI_TAXID=176299; [1]						
RN	SEQUENCE FROM N.A.						
RP	MEDLINE=21608551; PubMed=11743194;						
RX	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,						
RA	Houmeliel K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F.,						
RA	Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,						
RA	Flanagan C., Crowell C., Ginson J., Lemo C., Sear C., Strub G.,						
RA	Cielo C., Slater S.;						
RT	"Genome sequence of the plant pathogen and biotechnology agent						
RT	Agrobacterium tumefaciens C58. ;						
RT	Agrobacterium tumefaciens C58. ;						
RT	Science 294:2323-2328(2001).						
DR	EMBL; AE007981; AAC86253.1. ;						
SEQUENCE	103 AA; 11664 MW; 010BC2E7A865CAE7 CRC64;						
Query Match	100.0%; Score 21; DB 16; Length 103;						
Best Local Similarity	100.0%; Pred. No. 5.8e+02;						
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
RESULT 44							
Q8DF0	PRELIMINARY; PRT; 103 AA.						
ID	Q8DF0;						
AC	Q8DF0; PRELIMINARY; PRT; 103 AA.						
DT	01-JUN-2001 (TREMBREL 17, Last sequence update)						
DT	01-JUN-2001 (TREMBREL 17, Last annotation update)						
DE	AGR_C_774.						
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970).						
OC	Bacteria; Proteobacteria; alpha subdivision: Rhizobiaceae group;						
OC	Bacteria; Proteobacteria; Rhizobiaceae; Rhizobium.						
OX	NCBI_TAXID=176299; [1]						
RN	SEQUENCE FROM N.A.						
RP	MEDLINE=21608551; PubMed=11743194;						
RX	Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,						
RA	Houmeliel K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F.,						
RA	Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,						
RA	Flanagan C., Crowell C., Ginson J., Lemo C., Sear C., Strub G.,						
RA	Cielo C., Slater S.;						
RT	"Genome sequence of the plant pathogen and biotechnology agent						
RT	Agrobacterium tumefaciens C58. ;						
RT	Agrobacterium tumefaciens C58. ;						
RT	Science 294:2323-2328(2001).						
DR	EMBL; AE007981; AAC86253.1. ;						
SEQUENCE	103 AA; 11664 MW; 010BC2E7A865CAE7 CRC64;						
Query Match	100.0%; Score 21; DB 16; Length 103;						
Best Local Similarity	100.0%; Pred. No. 5.8e+02;						
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
RESULT 45							
Q8DF0	PRELIMINARY; PRT; 104 AA.						
ID	Q8DF0;						
AC	Q8DF0; PRELIMINARY; PRT; 104 AA.						
DT	01-JUN-2001 (TREMBREL 17, Last sequence update)						
DT	01-JUN-2001 (TREMBREL 17, Last annotation update)						
DE	AGR_C_774.						
OS	Agrobacterium tumefaciens (strain C58 / ATCC 33970).						
OC	Bacteria; Proteobacteria; alpha subdivision: Rhizobiaceae group;						
OC	Bacteria; Proteobacteria; Rhizobiaceae; Rhizobium.						
OX	NCBI_TAXID=100990; [1]						
RN	SEQUENCE FROM N.A.						
RP	MEDLINE=2108560; PubMed=11217851;						
RC	Strain=C57BL/6J;						
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,						
RA	Araiwa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,						
RA	Araiwa K., Izawa M., Nishi K., Kyrosawa H., Kondo S., Yamakawa I.,						
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,						
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cassavant T.,						
RA	Fleischmann R., Gaasterland T., Gissi C., King B., Kochiwa H.,						
RA	Kueli P., Lewis S., Matsuo Y., Niikido I., Pesole G., Quackenbush J.,						
RA	Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,						
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,						

RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Maslina J., Mazzarelli J., Mombaerts P...	RP	SEQUENCE FROM N.A.
RA	Nordone P., Ring B., Rindbach M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Suya T., Shiba Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;	RC	SJRAINCHPRSA;
RA	"Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690 (2001).	RT	The complete DNA sequence and transcription map of the unique long genome region of Marek's disease virus type 2.";
DR	EMBL: AK013746; BAA8981.1; -	RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR	MGD; MGI:1920284; 2900064; B16RIK.	DR	EMBL: AB024414; BAA8291.1; -.
SEQUENCE	104 AA; 11669 MW; 7BAD049EC63D6B0 CRC64;	FT	NON-TER 1
SQ	106 AA; 11066 MW; 275DF75DF3E15C39 CRC64;	SQ	SEQUENCE 106 AA; 11066 MW; 275DF75DF3E15C39 CRC64;
Query Match	100.0%; Score 21; DB 11; Length 104;	Query Match	100.0%; Score 21; DB 12; Length 106;
Best Local Similarity	100.0%; Pred. No. 5.9e+02;	Best Local Similarity	100.0%; Pred. No. 6e+02;
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 HARL 4	QY	1 HARL 4
ID	1111 4	ID	1111 37
Db	96 HARL 99	Db	34 HARL 37
RESULT 46		RESULT 48	
08QZYS	PRELIMINARY; PRT; 105 AA.	09P8A0	PRELIMINARY; PRT; 107 AA.
ID	08QZYS	ID	09P8A0
AC	08QZYS	AC	09P8A0:
DT	01-JUN-2002 (TREMBrel. 21, Created)	DT	01-MAR-2001 (TREMBrel. 16, Last sequence update)
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)	DT	01-MAR-2001 (TREMBrel. 16, Last annotation update)
DE	FUS2.	DE	M0BC.
OS	Mus musculus (Mouse).	OS	Escherichia coli.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.	OG	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX	NCBI_TaxID=10090;	OC	Escherichia.
RN	[1]	OX	NCBI_TaxID=562;
RP	SEQUENCE FROM N.A.	RN	[1]
RC	STRAIN=C129/SV;	RC	SEQUENCE FROM N.A.
RA	Shuttleworth T.L., Wilson M.D., Wicklow B.A., Wilkins J., Triggs-Raine B.L.;	RA	Zakharova M.V.;
RA	"Characterization of the Murine Hyaluronidase Gene Region Reveals Complex Organization and Co-transcription of Hyall with Downstream Genes, Fus2 and Hyall3"; J. Biol. Chem. 0:0-0(2002).	RT	Escherichia coli plasmid pLG13, complete sequence.";
RL	J. Biol. Chem. 0:0-0(2002).	RT	Escherichia coli plasmid pLG13, complete sequence.";
DR	EMBL: AF417493; AAC14423.1; -.	RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AF417497; AAC14431.1; -.	DR	EMBL: AF251289; AAC18127.1; -.
FT	NON_TER 105 105	FT	Plasmid
SQ	SEQUENCE 105 AA; 11522 MW; 859753EE6033F919 CRC64;	SQ	SEQUENCE 107 AA; 12019 MW; 15DE455470D720C7 CRC64;
Query Match	100.0%; Score 21; DB 11; Length 105;	Query Match	100.0%; Score 21; DB 2; Length 107;
Best Local Similarity	100.0%; Pred. No. 5.9e+02;	Best Local Similarity	100.0%; Pred. No. 6e+02;
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 HARL 4	QY	1 HARL 4
ID	1111 4	ID	11 HARL 14
Db	52 HARL 55	Db	11 HARL 14
RESULT 47		RESULT 49	
09QTE6	PRELIMINARY; PRT; 106 AA.	069423	PRELIMINARY; PRT; 107 AA.
ID	09QTE6	ID	069423
AC	09QTE6;	AC	069423;
DT	01-MAY-2000 (TREMBrel. 13, Created)	DT	01-AUG-1998 (TREMBrel. 07, Last sequence update)
DT	01-MAY-2000 (TREMBrel. 13, Last sequence update)	DT	01-AUG-1998 (TREMBrel. 07, Last sequence update)
DT	01-MAR-2002 (TREMBrel. 20, Last annotation update).	DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)
DE	Homolog of MDV1 PP24 protein (Fragment).	DE	M0BC.
OS	Marek's disease virus serotype 2 MDV2.	OS	Enterobacter cloacae.
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;	OC	Plasmid pCL18.
OC	Alphaherpesvirinae; Marek's disease-like viruses.	OC	Bacteria; Proteobacteriia; gamma subdivision; Enterobacteriaceae;
NCBI_TaxID=36303;		NCBI_TaxID=550;	
[1]		[1]	
..		..	
RN		RN	

KW Plasmid.
 SQ SEQUENCE 107 AA; 11886 MW; 1372246ACF372182 CRC64;
 Query Match 100.0%; Score 21; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy |||||
 1 HARL 4
 Db 11 HARL 14

RESULT 50

052252 PRELIMINARY; PRT; 107 AA.

ID 052252
 AC 052252
 DT 01-NOV-1996 (TREMBREL. 01, Created)
 DR 01-NOV-1996 (TREMBREL. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBREL. 19, Last annotation update)
 DE Mobilization protein.
 GN MBEC.
 OS *Salmonella enterica*.
 OG Plasmid pW0799.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Salmonella*.
 OX NCBI_TaxID=28901;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BORREZ;
 RX MEDLINE=95394842; PubMed=7545154;
 RA Keenleyside W.J., Whitfield C.;
 RT "Lateral transfer of rfb genes: a mobilizable ColE1-type plasmid
 carries the rfb034 (O:54 antigen biosynthesis) gene cluster from
 RT *Salmonella enterica* serovar Borreze.";
 RL J. Bacteriol. 177:5247-5253(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BORREZ;
 RX MEDLINE=97067086;
 RA Keenleyside W.J., Whitfield C.;
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 SQ SEQUENCE 107 AA; 11952 MW; 1372246CA737F7 CRC64;
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